

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:48:34 ; Search time 106.452 Seconds
(without alignments)
4565.212 Million cell updates/sec

Title: us-10-079-954-1
Perfect score: 297
Sequence: 1 gcaatcgatggggatcctt.....ccatcaagaagattatggt 297

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	3	US-09-308-984-1
2	282.8	95.2	933	3	US-08-808-148-2
3	282.8	95.2	1289	3	US-09-020-956-111
4	282.8	95.2	1289	3	US-09-030-607-111
5	282.8	95.2	1289	3	US-09-439-313-111
6	282.8	95.2	1289	3	US-09-352-616A-111
7	282.8	95.2	1289	3	US-09-232-149A-111
8	282.8	95.2	1289	4	US-09-159-812-111
9	282.8	95.2	1289	4	US-09-636-215-111
10	282.8	95.2	1289	4	US-09-685-166A-111
11	282.8	95.2	1289	4	US-09-115-453-111
12	282.8	95.2	1289	4	US-09-688-489-111
13	282.8	95.2	1289	4	US-09-679-426-111
14	282.8	95.2	1289	4	US-09-759-143-111
15	282.8	95.2	1289	4	US-09-651-236-111
16	282.8	95.2	1324	4	US-09-148-545-82
17	282.8	95.2	1376	4	US-09-148-545-14
18	272.8	91.9	740	3	US-09-020-956-17
19	272.8	91.9	740	3	US-09-030-607-17
20	272.8	91.9	740	3	US-09-439-313-17
21	272.8	91.9	740	3	US-09-352-616A-17
22	272.8	91.9	740	3	US-09-232-149A-17
23	272.8	91.9	740	4	US-09-159-812-17
24	272.8	91.9	740	4	US-09-636-215-17
25	272.8	91.9	740	4	US-09-685-166A-17
26	272.8	91.9	740	4	US-09-115-453-17
27	272.8	91.9	740	4	US-09-688-489-17

28	272.8	91.9	740	4	US-09-679-426-17	Sequence 17, Appl
29	272.8	91.9	740	4	US-09-759-143-17	Sequence 17, Appl
30	272.8	91.9	740	4	US-09-651-236-17	Sequence 17, Appl
31	263.8	88.8	729	3	US-09-020-956-13	Sequence 13, Appl
32	263.8	88.8	729	3	US-09-030-607-13	Sequence 13, Appl
33	263.8	88.8	729	3	US-09-439-313-13	Sequence 13, Appl
34	263.8	88.8	729	3	US-09-352-616A-13	Sequence 13, Appl
35	263.8	88.8	729	3	US-09-232-149A-13	Sequence 13, Appl
36	263.8	88.8	729	4	US-09-159-812-13	Sequence 13, Appl
37	263.8	88.8	729	4	US-09-636-215-13	Sequence 13, Appl
38	263.8	88.8	729	4	US-09-685-166A-13	Sequence 13, Appl
39	263.8	88.8	729	4	US-09-115-453-13	Sequence 13, Appl
40	263.8	88.8	729	4	US-09-688-489-13	Sequence 13, Appl
41	263.8	88.8	729	4	US-09-679-426-13	Sequence 13, Appl
42	263.8	88.8	729	4	US-09-759-143-13	Sequence 13, Appl
43	263.8	88.8	729	4	US-09-651-236-13	Sequence 13, Appl
C 44	220.6	74.3	801	3	US-09-020-956-16	Sequence 16, Appl
C 45	220.6	74.3	801	3	US-09-030-607-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-308-984-1
; Sequence 1, Application US/09308984
; Patent No. 6388065
; GENERAL INFORMATION:
; APPLICANT: Durst, Matthias
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/09/308,984
; CURRENT FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-308-984-1

Query Match 100.0%; Score 297; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCAATCGATGGGCATCCTTTCTGAAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAG	60
Db	1	GCAATCGATGGGCATCCTTTCTGAAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAG	60
Qy	61	TTTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGTCTTTGCTCTTGGTTTC	120
Db	61	TTTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGTCTTTGCTCTTGGTTTC	120
Qy	121	CTGGGCTGCTATGCTGTAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATC	180
Db	121	CTGGGCTGCTATGCTGTAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATC	180
Qy	181	CTCCTCTCATCTTTCATTGCTGAGTTGTCAGTCTGCTGGTTCGCTTGGTGACACCAT	240
Db	181	CTCCTCTCATCTTTCATTGCTGAGTTGTCAGTCTGCTGGTTCGCTTGGTGACACCAT	240
Qy	241	ATGCTGAGCACTTCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAAGATTATGTT	297
Db	241	ATGCTGAGCACTTCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAAGATTATGTT	297

RESULT 2
US-08-808-148-2
; Sequence 2, Application US/08808148

BEST AVAILABLE COPY

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 61
DB CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 121
DB TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 339
QY 122 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 181
DB TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 399
QY 182 TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 241
DB TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 459
QY 242 TGGCTGACACTTCCGAGCTTGCTGCTGCTAGTGCCTGCCATCAAGAA 287
DB TGGCTGACACTTCCGAGCTTGCTGCTGCTAGTGCCTGCCATCAAGAA 505

RESULT 10

US-09-685-166A-111
; Sequence 111, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 86-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 61
220 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 279
62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 121
280 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 339
122 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 181
340 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 399
182 TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 241

US-09-685-166A-111
; Sequence 111, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-685-166A-111

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 86-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 61
220 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 279
62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 121
280 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 339
122 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 181
340 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 399
182 TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 241

DB 400 TCTCTCATCTTCATTCGTGAGGTTGCAGCTGCTGTCGTCCAGTGCCATGCAGT 459
QY 242 TGGCTGAGCACTTCCGAGCTTGCTGCTAGTGCCTGCCATCAAGAA 287
DB 460 TGGCTGAGCACTTCCGAGCTTGCTGCTAGTGCCTGCCATCAAGAA 505

RESULT 11

US-09-115-453-111
; Sequence 111, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-115-453-111

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 86-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 61
220 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCACATGTCGTCCAGTGCCATGCAGT 279
62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 121
280 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGGCTTGTCGTCTTTGCTTTGGTTTC 339
122 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 181
340 TGGGCTGCTATGCTATAGACTGAGACGAAGTGTCCTCGTGAGCTTCTTCTTCATCC 399
182 TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 241
400 TCTCTCATCTTCATTCGTGAGGTTGCAGTCTGTCGTGTCGCTTTGGTGTACACATAA 459
242 TGGCTGAGCACTTCCGAGCTTGCTGCTGCTAGTGCCTGCCATCAAGAA 287
460 TGGCTGAGCACTTCCGAGCTTGCTGCTGCTAGTGCCTGCCATCAAGAA 505

RESULT 12

US-09-688-489-111
; Sequence 111, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-688-489-111

RESULT 15

US-09-651-236-111
; Sequence 111, Application US/09651236
; Patent No. 6818751

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-111

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	2	CAATCGATGGGGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGATGCACT 61
Db	220	CAATCGATGGGGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGATGCACT 279
QY	62	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGGCTTGGTCTTTGGCTCTTGGTTTCC 121
Db	280	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGGCTTGGTCTTTGGCTCTTGGTTTCC 339
QY	122	TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGCCTCGTGACGTTCTTCTTCATCC 181
Db	340	TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGCCTCGTGACGTTCTTCTTCATCC 399
QY	182	TCTCTCTCATCTTCATGCTGAGGTTGACAGTGTGCTGTGCTTGGCTTGGTGACACATAA 241
Db	400	TCTCTCTCATCTTCATGCTGAGGTTGACAGTGTGCTGTGCTTGGCTTGGTGACACACAA 459
QY	242	TGGCTGAGCAGTCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 287
Db	460	TGGCTGAGCAGTCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 505

Search completed: August 27, 2005, 11:37:05
Job time : 107.452 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:00:48 ; Search time 355.016 Seconds
(without alignments)
4952.347 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatggggcattcctt.....ccatcaagaattatggtt 297

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	2	Aav15588 Human HPK
2	282.8	95.2	513	5	Aaf93382 Lung carc
3	282.8	95.2	635	4	Aai29471 Colon tum
4	282.8	95.2	635	8	Abz33657 Human col
5	282.8	95.2	792	6	Abk29835 Colon ade
6	282.8	95.2	933	2	Aav54014 Nucleotid
7	282.8	95.2	1076	6	Abz76533 cDNA enco
8	282.8	95.2	1076	10	Abz75600 Prostate
9	282.8	95.2	1076	13	Adz25330 Breast ca
10	282.8	95.2	1076	13	Adz65868 Human pro
11	282.8	95.2	1076	13	Adz66771 Human tum
12	282.8	95.2	1154	6	Abz76532 cDNA enco
13	282.8	95.2	1154	10	Abz75598 Prostate
14	282.8	95.2	1278	11	Adn39285 Cancer/an
15	282.8	95.2	1288	2	Aav48113 Nucleotid
16	282.8	95.2	1288	10	Adz62626 DNA #4 us
17	282.8	95.2	1288	10	Adz62609 Human rec
18	282.8	95.2	1289	2	Aav58587 Prostate
19	282.8	95.2	1289	2	Aav58587 Prostate
20	282.8	95.2	1289	2	Aav61202 Full leng

21	282.8	95.2	1289	3	ABs71255	Human pro
22	282.8	95.2	1289	4	AAH93466	Human pro
23	282.8	95.2	1289	4	AAH93466	Human pro
24	282.8	95.2	1289	4	AAH02531	Prostate
25	282.8	95.2	1289	4	AAH84780	Human pro
26	282.8	95.2	1289	4	AAH84780	Human pro
27	282.8	95.2	1289	5	ACA59367	Prostate
28	282.8	95.2	1289	5	AAH10109	Human pro
29	282.8	95.2	1289	6	ABL94930	Human Ni-
30	282.8	95.2	1289	6	ABs58639	Prostate
31	282.8	95.2	1289	8	ACC95094	Prostate
32	282.8	95.2	1289	10	ADBI3561	Human pro
33	282.8	95.2	1289	10	ADG25977	Human pro
34	282.8	95.2	1290	3	AAA06350	Human imm
35	282.8	95.2	1306	13	ADR44012	Human bre
36	282.8	95.2	1324	2	AAV34225	Human sec
37	282.8	95.2	1324	8	ACD08096	cDNA enco
38	282.8	95.2	1376	2	AAV34157	Human sec
39	282.8	95.2	1376	8	ACD08028	cDNA enco
40	282.8	95.2	1456	9	ADA11015	Human cDN
41	282.8	95.2	1533	3	AAZ95011	Cancer sp
42	282.8	95.2	1603	5	ABV23358	Human pro
43	282.8	95.2	1603	5	ADL62990	Human ova
44	282.8	95.2	1605	2	AAV30916	Human sec
45	282.8	95.2	1605	5	AAF98395	Human cDN

ALIGNMENTS

RESULT 1

AAV15588
ID AAV15588 standard; DNA; 297 BP.

XX AAV15588;

XX 02-JUL-1998 (first entry)

XX Human HPK-1A C4.8 DNA.

XX Cervical cancer; treatment; diagnosis; passage cell; lesion;
XX human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

XX Homo sapiens.

XX DE19649207-C1.

XX 26-FEB-1998.

XX 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;

XX WPI; 1998-121623/12.

XX P-PSDB; AAW47275.

XX Nucleic acid characteristic of late or early passage cells immortalised
XX by papilloma virus - and related polypeptide(s) and antibodies, used for
XX diagnosis and treatment of cervical cancer and assessing potential for
XX progression of cervical lesions.

XX Claim 2; Fig 1; 8pp; German.

XX This sequence, C4.8, is derived from a human papillomavirus (HPV)

XX immortalised human foreskin keratinocyte cell line HPK-1A and is
XX characteristic of late or early passage cells. This sequence is used in a
XX method for assessing the potential for progression of cervical lesions.

XX Antibodies generated against the encoded polypeptide are used for
XX diagnosis of cervical cancer and to assess potential for lesion

PT Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer.

XX Claim 2; Page 414; 472pp; English.

XX The present invention describes colon tumor associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumor associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI29460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention

XX Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;

Query Match 95.2%; Score 282.8; DB 4; Length 635;

Best Local Similarity 99.3%; Pred. No. 7.8e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 61

DB 575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 516

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGTGCTTGTGCTTGTGTTTCC 121

DB 515 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGTGCTTGTGCTTGTGTTTCC 456

QY 122 TGGGCTGCTATGCTGCTAGACTGAGCAAGTGCCCTCGTGAGCTTCTTTCATCC 181

DB 455 TGGGCTGCTATGCTGCTAGACTGAGCAAGTGCCCTCGTGAGCTTCTTTCATCC 396

QY 182 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241

DB 395 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336

QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287

DB 335 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290

RESULT 4

ABZ33657/c

ID ABZ33657 standard; cDNA; 635 BP.

XX ABZ33657;

XX 30-JAN-2003 (first entry)

DT Human colon tumour cDNA for clone R0098:F06 SEQ ID NO:1025.

DE Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer; tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.

OS Homo sapiens.

XX WO200283070-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US011475.

XX 10-APR-2001; 2001US-00833263.

PR 03-AUG-2001; 2001US-00922217.

PR 19-DEC-2001; 2001US-00025380.

XX (CORI-) CORIXA CORP.

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;

PI Fanger GR, Vedvick TS, Carter D;

XX WPI; 2003-067548/06.

XX New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer.

PS Disclosure; Page 415; 537pp; English.

XX The present invention describes compounds (I) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; and (6) a method for inhibiting the development of cancer in a patient. (I) have immunostimulant and cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725 and ABP55343 to ABP55391 represent human colon cancer/tumour related sequences used in the exemplification of the present invention

XX Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;

Query Match 95.2%; Score 282.8; DB 8; Length 635;

Best Local Similarity 99.3%; Pred. No. 7.8e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 61

DB 575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 516

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGTGCTTGTGCTTGTGTTTCC 121

DB 515 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGTGCTTGTGCTTGTGTTTCC 456

QY 122 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTCCTCGTGAGCTTCTTTCATCC 181

DB 455 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTCCTCGTGAGCTTCTTTCATCC 396

QY 182 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241

DB 395 TCCTCCTCATCTTCAATGCTGAGGTTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336

QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287

DB 335 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290

RESULT 5

ABK29835

ID ABK29835 standard; cDNA; 792 BP.

XX ABK29835;

XX 23-APR-2002 (first entry)

XX Colon adenocarcinoma-specific cDNA #361.

DE Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.

XX

OS Homo sapiens.
PN WO200196389-A2.
XX 20-DEC-2001.
PD
XX 07-JUN-2001; 2001WO-US018574.
PF
XX 09-JUN-2000; 2000US-0210667P.
PR 22-NOV-2000; 2000US-0252614P.
XX (CORI-) CORIXA CORP.
PA
PI Meagher MJ, King GE, Xu J, Secrist H;
XX WPI; 2002-098052/13.
DR
XX New isolated polynucleotide encoding a polypeptide comprising a portion
PT of colon tumor protein, for detection, diagnosis and therapy of human
PT colon cancer.
PT
XX
PS Claim 1; Page 207; 21lpp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a
CC polypeptide (II) comprising a portion of a colon tumor protein. A new
CC oligonucleotide (III) that hybridises to (I) is useful for determining
CC the presence of a cancer in a patient. (II) or antigen presenting cells
CC expressing (I) are useful for stimulating and/or expanding T cells
CC specific for a tumor protein, by contacting T cells with (I), (II) or
CC antigen-presenting cells that express (I), (II), or antigen
CC presenting cells that express (II) are useful for treating colon cancer
CC in a patient by incubating CD4+ and/or CD8+ T cells isolated from a
CC patient with (I), (II), or antigen presenting cells that express (II), so
CC that T cells proliferate, and administering to the patient an effective
CC amount of the proliferated T cells, thus inhibiting the development of a
CC cancer in the patient. A new composition is useful for stimulating an
CC immune response in a patient. (I) or (II) is useful in vaccines and
CC pharmaceutical compositions for prevention and treatment of colon cancer
CC and for the diagnosis and monitoring of the cancers. (I), (II) or an
CC antibody against (II) is useful for detection, diagnosis and/or therapy
CC of human colon cancer. (I) is useful as a probe or primer for nucleic
CC acid hybridisation, and in the design and preparation of ribozyme
CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of
CC the invention
XX
SQ Sequence 792 BP; 165 A; 218 C; 197 G; 212 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 6; Length 792;
Best Local Similarity 99.3%; Pred. No. 8.4e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 214 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 273
QY 62 TTGTCAAGTGGGCTACTTCTTCATCGCAGCGGGGTGTGTCTTGTCTTGTGTTTCC 121
DB 274 TTGTCAAGTGGGCTACTTCTTCATCGCAGCGGGGTGTGTCTTGTCTTGTGTTTCC 333
QY 122 TGGGCTGCTATGCTGCTAAGACTGAGACAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 181
DB 334 TGGGCTGCTATGCTGCTAAGACTGAGACAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 393
QY 182 TCCTCTCATCTTCATTTGCTGAGTGTGACGTGCTGTGTGTCGCTTGTGTACACATAA 241
DB 394 TCCTCTCATCTTCATTTGCTGAGTGTGACGTGCTGTGTGTCGCTTGTGTACACATAA 453
QY 242 TGGCTGAGCATTCCGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 287
DB 454 TGGCTGAGCATTCCCTGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 499

RESULT 6
AAV54014
ID AAV54014 standard; cDNA; 933 BP.
XX
XX AAV54014;
XX
XX 02-DEC-1998 (first entry)
XX
XX Nucleotide sequence of the human tumour-associated antigen.
XX
XX Human; tumour-associated antigen; PRAT; stimulation; cell proliferation;
XX antagonist; cancer; genetic defect; sickle cell anaemia; agonist;
XX antibody; hybridisation; probe; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 128..855
CDS /*tag= a
FT /*tag= a
FT /product= "human tumour-associated antigen"
XX
XX WO9838310-A1.
XX
XX 03-SEP-1998.
XX
XX 27-FEB-1998; 98WO-US003953.
XX
XX 28-FEB-1997; 97US-00808148.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Hillman JL, Goli SK;
XX
XX WPI; 1998-481208/41.
DR P-ESDB; AAW59954.
XX
XX Human tumour-associated antigen PRAT - useful for stimulating cell
PT proliferation and screening for antagonists useful to treat or prevent
PT cell proliferation disorders e.g. cancers.
XX
XX Disclosure; Fig 1A-1C; 54pp; English.
XX
XX This is the nucleotide sequence of the human tumour-associated antigen
CC (PRAT) used in the method of the invention for stimulating cell
CC proliferation and screening for antagonists useful to treat or prevent
CC cell proliferation disorders such as cancer, and genetic defect e.g.
CC sickle cell anaemia. The polypeptides can be combined with a suitable
CC carrier in pharmaceutical compositions, and also used to screen for
CC antagonists, agonists, and to generate antibodies. PRAT agonists can be
CC added to a cell to stimulate cell proliferation by increasing or
CC prolonging the activity of PRAT as above. The antagonists can be combined
CC with a suitable carrier in pharmaceutical compositions, which can be
CC administered to subjects to treat or prevent disorders associated with
CC cell proliferation, especially cancers. Antibodies specific for PRAT may
CC be used directly as antagonists, or indirectly as a targeting or delivery
CC mechanism to bring pharmaceutical agents to PRAT-expressing cells. They
CC are also useful to diagnose conditions or diseases characterised by PRAT
CC expression and to monitor therapeutic interventions. The polynucleotide
CC encoding PRAT, or complementary sequences, can be used to produce
CC hybridisation probes, useful to detect polynucleotides or fragments
CC encoding PRAT, e.g. to diagnose diseases relating to polypeptide
XX expression or monitor PRAT regulation during therapeutic intervention
XX
SQ Sequence 933 BP; 198 A; 254 C; 236 G; 245 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 2; Length 933;
Best Local Similarity 99.3%; Pred. No. 9e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 225 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 284

sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 13; Length 1076;
Best Local Similarity 99.3%; Pred. No. 9.4e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB |||||||
QY 62 TTGTCAAGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTGGTTTCC 121
DB |||||||
QY 158 TTGTCAAGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTGGTTTCC 217
DB |||||||
QY 122 TGGGCTGCTATGGTCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB |||||||
QY 218 TGGGCTGCTATGGTCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCATTCGTGAGGTTGCAAGTGTGTTGGTGCCTTGGTGACCAAPAA 241
DB |||||||
QY 278 TCCTCCTCATCTTCATTCGTGAGGTTGCAAGTGTGTTGGTGCCTTGGTGACCAACAA 337
QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB |||||||
QY 338 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

RESULT 12

ADO85081
ID ADO85081 standard; cDNA; 1077 BP.

XX
AC ADO85081;

XX
DT 07-OCT-2004 (first entry)

XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1895.

XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.

XX
OS Homo sapiens.

XX
PN WO2004060270-A2.

XX
PD 22-JUL-2004.

XX
PF 15-OCT-2003; 2003WO-US029126.

XX
PR 18-OCT-2002; 2002US-0418988P.

XX
PA (GETH) GENENTECH INC.

XX
PA (WUTD/) WU T D.

XX
PA (ZHOU/) ZHOU Y.

XX
PI Wu TD, Zhou Y;

XX
DR WPI; 2004-534300/51.

XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.

XX
PS Claim 1; SEQ ID NO 1895; 5504pp; English.

XX

The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC the presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX

SQ Sequence 1077 BP; 227 A; 279 C; 282 G; 289 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 13; Length 1077;

Best Local Similarity 99.3%; Pred. No. 9.4e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61

DB |||||||

QY 98 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157

DB |||||||

QY 62 TTGTCAAGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTGGTTTCC 121

DB |||||||

QY 158 TTGTCAAGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTGGTTTCC 217

DB |||||||

QY 122 TGGGCTGCTATGGTCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181

DB |||||||

QY 218 TGGGCTGCTATGGTCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277

QY 182 TCCTCCTCATCTTCATTCGTGAGGTTGCAAGTGTGTTGGTGCCTTGGTGACCAATAA 241

DB |||||||

QY 278 TCCTCCTCATCTTCATTCGTGAGGTTGCAAGTGTGTTGGTGCCTTGGTGACCAACAA 337

QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287

DB |||||||

QY 338 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 383

RESULT 13

ABS76532

ID ABS76532 standard; cDNA; 1154 BP.

XX
AC ABS76532;

XX
DT 11-DEC-2002 (first entry)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:03:53 ; Search time 1577.61 Seconds
(without alignments)
9122.136 Million cell updates/sec

Title: US-10-079-954-1
Perfect score: 297
Sequence: 1 gcaatcgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 47082233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hq:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_scs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	297	100.0	297	6	A91802	A91802 Sequence 1
2	297	100.0	297	6	BD023236	BD023236 DNA for e
3	282.8	95.2	513	6	AX079459	AX079459 Sequence
C	282.8	95.2	635	6	AX193458	AX193458 Sequence
5	282.8	95.2	792	6	AX379319	AX379319 Sequence
6	282.8	95.2	933	6	BD070552	BD070552 Novel hum
7	282.8	95.2	1044	9	AF133425	AF133425 Homo sapi
8	282.8	95.2	1076	9	AF054838	AF054838 Homo sapi
9	282.8	95.2	1077	6	C0719831	C0719831 Sequence
10	282.8	95.2	1278	9	AF065388	AF065388 Homo sapi
11	282.8	95.2	1288	6	BD069061	BD069061 Polynucle
C	282.8	95.2	1288	6	BD069078	BD069078 Polynucle
13	282.8	95.2	1289	6	BD242023	BD242023 Compounds
14	282.8	95.2	1289	6	AR237206	AR237206 Sequence
15	282.8	95.2	1289	6	AR278230	AR278230 Sequence
16	282.8	95.2	1289	6	AR366926	AR366926 Sequence
17	282.8	95.2	1289	6	AR370822	AR370822 Sequence
18	282.8	95.2	1289	6	AR392327	AR392327 Sequence
19	282.8	95.2	1289	6	AR399962	AR399962 Sequence

20	282.8	95.2	1289	6	AR405229	AR405229 Sequence
21	282.8	95.2	1289	6	AR439433	AR439433 Sequence
22	282.8	95.2	1289	6	AR563609	AR563609 Sequence
23	282.8	95.2	1289	6	AX106213	AX106213 Sequence
24	282.8	95.2	1289	6	AX106330	AX106330 Sequence
25	282.8	95.2	1289	6	AX140621	AX140621 Sequence
26	282.8	95.2	1289	6	AX200481	AX200481 Sequence
27	282.8	95.2	1289	6	AX267137	AX267137 Sequence
28	282.8	95.2	1289	6	BD070259	BD070259 Compounds
29	282.8	95.2	1297	9	BC007290	BC007290 Homo sapi
30	282.8	95.2	1297	9	BC013404	BC013404 Homo sapi
31	282.8	95.2	1324	6	BD195620	BD195620 70 human
32	282.8	95.2	1324	6	CQ775665	CQ775665 Sequence
33	282.8	95.2	1324	6	AR352675	AR352675 Sequence
34	282.8	95.2	1376	6	BD195552	BD195552 70 human
35	282.8	95.2	1376	6	CQ775597	CQ775597 Sequence
36	282.8	95.2	1376	6	AR352607	AR352607 Sequence
37	282.8	95.2	1533	6	BD228312	BD228312 Method of
38	282.8	95.2	1603	6	CQ414131	CQ414131 Sequence
39	282.8	95.2	1603	6	CQ491480	CQ491480 Sequence
40	282.8	95.2	1605	6	BD190734	BD190734 Secreted
41	282.8	95.2	1605	6	AX099394	AX099394 Sequence
C 42	281.8	94.9	601	6	AX193317	AX193317 Sequence
C 43	281.8	94.9	693	6	AX193383	AX193383 Sequence
C 44	280.8	94.5	649	6	AX193358	AX193358 Sequence
45	278	93.6	471	6	BD139381	BD139381 Extended

ALIGNMENTS

RESULT 1
A91802
LOCUS: A91802 297 bp DNA linear PAT 22-JAN-2000
DEFINITION: Sequence 1 from Patent WO9823775.
ACCESSION: A91802
VERSION: A91802.1 GI:6740681
KEYWORDS: unidentified
SOURCE: unidentified
ORGANISM: unclassified.
REFERENCE: 1 (bases 1 to 297)
AUTHORS: Nees,M. and Duerst,M.
TITLE: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL: Patent: WO 9823775-A 1 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
FEATURES
source
1..297
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
<1..>297
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69434.1"
/db_xref="GI:6740682"
/translation="AIDGASFLKIFGPISSSMQFVNVGVFLIAGVVFALGELCY
GAKTESKCALVTFPFFILLIFIAEVAALVALVTIIMAEHPFLVLVPAIKIMV"

CDS

ORIGIN

Query Match 100.0%; Score 297; DB 6; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.2e-68;
Matches: 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAATCGATGGGGCATCTTTCTGAAGACTTCGCGGCACCTGTCTCGTCAGTCCCATGCAG 60
Db 1 GCAATCGATGGGGCATCTTTCTGAAGACTTCGCGGCACCTGTCTCGTCAGTCCCATGCAG 60
Qy 61 TTTTGTCAACGTGGGCTACTTCTCTCATCGACCGCGGTGTGGTCTTTGCTTTGGTTTC 120
Db 61 TTTTGTCAACGTGGGCTACTTCTCTCATCGACCGCGGTGTGGTCTTTGCTTTGGTTTC 120
Qy 121 CTGGGCTGTATGTGTGCTAAGACTGAGCAAGTGTGCCCTCGTGCCTTCTTCTTCATC 180

```

|||||
121 CTGGCTGCTATGTTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
QY 181 CTCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 240
Db 181 CTCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 240
QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297

RESULT 2
BD023236 297 bp DNA linear PAT 27-AUG-2002
LOCUS BD023236
DEFINITION DNA for evaluating progress potential of cervical diseases.
ACCESSION BD023236
VERSION BD023236.1 GI:22564459
KEYWORDS JP 2001504703-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Durst M. and Ness M.
TITLE DNA for evaluating progress potential of cervical diseases
JOURNAL Patent: JP 2001504703-A 1 10-APR-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT PN JP 2001504703-A/1
PD 10-APR-2001
PF 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19649207.6
PI MATHIAS DURST; MATHIAS NESS
PC C12N15/09, C07K14/00, C07K16/00, C12P21/02, C12Q1/68, C12Q1/70, PC
GOIN33/574,
PC C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 1..297
FEATURES source
1..297
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 297; DB 6; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.2e-68;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAG 60
Db 1 GCAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAG 60
QY 61 TTGTGCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTC 120
Db 61 TTGTGCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTC 120
QY 121 CTGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATC 180
Db 121 CTGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATC 180
QY 181 CTCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 240
Db 181 CTCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 240
QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297

RESULT 3
Query Match 95.2%; Score 282.8; DB 6; Length 635;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAGT 61
Db 99 CAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAGT 158
QY 62 TTGTCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTCC 121
Db 159 TTGTCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTCC 218
QY 122 TGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATCC 181
Db 219 TGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATCC 278
QY 182 TCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 241
Db 279 TCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 338
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 384

RESULT 4
AX193458/c
LOCUS AX193458
DEFINITION Sequence 1025 from Patent WO0149716.
ACCESSION AX193458
VERSION AX193458.1 GI:15211409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
Stolk, J.A., King, G.E., Wang, T., and Jiang, Y.
TITLE Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
JOURNAL Patent: WO 0149716-A 1025 12-JUL-2001;
CORIXA CORPORATION (US)
FEATURES source
1..635
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 635;

```

```

AX079459
LOCUS AX079459
DEFINITION Sequence 203 from Patent WO0107611.
ACCESSION AX079459
VERSION AX079459.1 GI:13159019
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Goddard, A. and Wood, W.I.
TITLE Human polypeptides and methods for the use thereof
JOURNAL Patent: WO 0107611-A 203 01-FEB-2001;
Genentech, Inc. (US)
FEATURES source
1..513
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 513;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAGT 61
Db 99 CAATCGATGGGGCATCTTCTTGAAGATCTTCGGGGCACTGTCTCCAGTGCCCATGCAGT 158
QY 62 TTGTCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTCC 121
Db 159 TTGTCAACGTGGGCTACTCTCTCATCCAGCCGCGTTGGTCTTGTCTTGGTTTCC 218
QY 122 TGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATCC 181
Db 219 TGGCTGCTATGTTGCTAAGACTGAGACGAAGTGTGCCCTCGTACGCTTCTTCTTCATCC 278
QY 182 TCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 241
Db 279 TCCTCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATTA 338
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 384

RESULT 4
AX193458/c
LOCUS AX193458
DEFINITION Sequence 1025 from Patent WO0149716.
ACCESSION AX193458
VERSION AX193458.1 GI:15211409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
Stolk, J.A., King, G.E., Wang, T., and Jiang, Y.
TITLE Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
JOURNAL Patent: WO 0149716-A 1025 12-JUL-2001;
CORIXA CORPORATION (US)
FEATURES source
1..635
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 635;

```

Qy 242 TGGCTGAGCACCCTCCGACGTTGCTGGTAGTGCTGCCATCAAGAA 287
|||||
Db 454 TGGCTGAGCACCTTCTGACGTTGCTGGTAGTGCTGCCATCAAGAA 499

SOURCE	ORGANISM	REFERENCE	AUTHORS
1			
M			
E			
H			
I			

AF133425 1044 bp mRNA linear PRI 16-NOV-1999
Homo sapiens tetraspanin TW4-C mRNA, complete cds.
AF133425
AF133425.1 GI:6434903
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1044)
Puls,K.L., Ni,J., Liu,D., Morahan,G. and Wright,M.D.

TITLE		The molecular characterization of four tetraspanins	
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1044)		
TITLE	Puls,K.L., Ni,J., Liu,D. and Wright,M.D.		
JOURNAL	Submitted (08-MAR-1999) Immunology, The Walter & Eliza Hall Institute, Royal Parade, Parkville, Victoria 3031, Australia		
FEATURES	Location/Qualifiers		
source	1..1044		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	124..849		
	/note="transmembrane 4 superfamily member"		
	/codon_start=1		
	/product="tetraspanin TM4-C"		
	/protein_id="AAF08364.1"		
	/db_xref="GI:6434904"		
	/translation="MQCFSPFKTMWILFNLLIFLCGAALLAVGIWVSIDGASFLKIFG PLSSAMQFVNVGYFLIAGVVFALGFLGCGYKTESKCALVTFIFILLILIFAEVA AAVALVYTTMAEHFLTLLVPAIKDYGSQEDFTQVWNTMKGLKCCGFTNYTDFED SPYFKNSAFPFCNDNVNTANETCTKQKAHDQKVEGCFNQLLDYDRTNAVTGGV AAGIGGLELAAMIVSMYLCNLQ"		
ORIGIN			
	Query Match 95.2%; Score 282.8; DB 9; Length 1044;		
	Best Local Similarity 99.3%; Pred. No. 1.4e-64;		
	Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61		
DB	221 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 280		
QY	62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 121		
DB	281 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 340		
QY	122 TGGGCTGCTATGCTGCTAGACTGAGACCAAGTGCCTCGTACGCTTCTTCTTCATCC 181		
DB	341 TGGGCTGCTATGCTGCTAGACTGAGACCAAGTGCCTCGTACGCTTCTTCTTCATCC 400		
QY	182 TCCTCTCATCTTCAATGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCAATAA 241		
DB	401 TCCTCTCATCTTCAATGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCAATAA 460		
QY	242 TGGCTGAGCACTTCGGAGCTTCTGGTAGTGCCTGCCATCAAGAA 287		
DB	461 TGGCTGAGCACTTCGGAGCTTCTGGTAGTGCCTGCCATCAAGAA 506		
RESULT 8			
AF054838			
LOCUS	AF054838 1076 bp mRNA linear PRI 03-NOV-1998		
DEFINITION	Homo sapiens tetraspan TM4SF (TSPAN-1) mRNA, complete cds.		
ACCESSION	AF054838		
VERSION	AF054838.1 GI:2997740		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1076)		
AUTHORS	Todd,S.C., Doctor,V.S. and Levy,S.		
TITLE	Sequences and expression of six new members of the tetraspanin/TW4SF family		
JOURNAL	Biochim. Biophys. Acta 1399 (1), 101-104 (1998)		
MEDLINE	98390278		
PUBMED	9714763		
REFERENCE	2 (bases 1 to 1076)		
AUTHORS	Todd,S.C., Doctor,V.S. and Levy,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-MAR-1998) Medicine, Stanford, 300 Pasteur, Stanford, CA 94305-5115, USA		

FEATURES		Location/Qualifiers	
source	1..1076		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
gene	1..1076		
	/gene="TSPAN-1"		
CDS	1..726		
	/gene="TSPAN-1"		
	/note="tetraspanin; transmembrane 4 super family; Tspan-1"		
	/codon_start=1		
	/product="tetraspan TM4SF"		
	/protein_id="AAC69714.1"		
	/db_xref="GI:2997741"		
	/translation="MQCFSPFKTMWILFNLLIFLCGAALLAVGIWVSIDGASFLKIFG PLSSAMQFVNVGYFLIAGVVFALGFLGCGYKTESKCALVTFIFILLILIFAEVA AAVALVYTTMAEHFLTLLVPAIKDYGSQEDFTQVWNTMKGLKCCGFTNYTDFED SPYFKNSAFPFCNDNVNTANETCTEOKAHDQKVEGCFNQLLDYDRTNAVTGGV AAGIGGLELAAMIVSMYLCNLQ"		
ORIGIN			
	Query Match 95.2%; Score 282.8; DB 9; Length 1076;		
	Best Local Similarity 99.3%; Pred. No. 1.4e-64;		
	Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61		
DB	98 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157		
QY	62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTTGTGTCCTTTGGTTTCC 121		
DB	158 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTTGTGTCCTTTGGTTTCC 217		
QY	122 TGGGCTGCTATGCTGCTAGACTGAGACCAAGTGCCTCGTACGCTTCTTCTTCATCC 181		
DB	218 TGGGCTGCTATGCTGCTAGACTGAGACCAAGTGCCTCGTACGCTTCTTCTTCATCC 277		
QY	182 TCCTCTCATCTTCAATGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 241		
DB	278 TCCTCTCATCTTCAATGCTGAGGTTCGAGCTGCTGTGGTGCCTTGGTGACACCAATAA 337		
QY	242 TGGCTGAGCACTTCGGAGCTTCTGGTAGTGCCTGCCATCAAGAA 287		
DB	338 TGGCTGAGCACTTCGGAGCTTCTGGTAGTGCCTGCCATCAAGAA 383		
RESULT 9			
CQ719831			
LOCUS	CQ719831 1077 bp DNA linear PAT 03-FEB-2004		
DEFINITION	Sequence 5765 from Patent WO02068579.		
ACCESSION	CQ719831		
VERSION	CQ719831.1 GI:42280688		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.		
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof		
JOURNAL	Patent: WO 02068579-A 5765 06-SEP-2002;		
	PE Corporation (NY) (US)		
FEATURES	Location/Qualifiers		
source	1..1077		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
	Query Match 95.2%; Score 282.8; DB 6; Length 1077;		
	Best Local Similarity 99.3%; Pred. No. 1.4e-64;		

[illegible]

QY 242 TGGCTGAGCATTCCGCGCTTGTGCTAGTGCCTGCCATCAAGAA 287
|||||
Db 455 TGGCTGAGCATTCTCGCTTGTGCTAGTGCCTGCCATCAAGAA 500
|||||

RESULT 12
BD069078/c
LOCUS BD069078 1288 bp DNA linear PAT 27-AUG-2002
DEFINITION Polynucleotides and polypeptides encoding receptors.
ACCESSION BD069078
VERSION JP 2001509679-A/21.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 1288)
AUTHORS Ni,J., Gentz,R.L. and Rosen,C.A.
TITLE Polynucleotides and polypeptides encoding receptors
JOURNAL Patent: JP 2001509679-A 21 24-JUL-2001;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001509679-A/21
PD 24-JUL-2001
PF 21-JAN-1998 JP 1998534602
PR 21-JAN-1997 US 60/034204,21-JAN-1997 US 60/034205 PI
JIAN NI, REINER L GENTZ, CRAIG A ROSEN
PC C12N15/12, C12N15/85, C12N5/10, C07K14/705, C07K16/28, C12Q1/68, PC
A61K38/17,
PC A61K48/00
CC Strandedness: Single;
CC Topology: Linear;
CC Polynucleotides and polypeptides encoding receptors FH Key
FT source 1..1288
FT /organism='Unidentified'.
FEATURES
source
1..1288
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1288;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
|||||
Db 1074 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 1015
|||||

QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 121
|||||
Db 1014 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 955
|||||

QY 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
|||||
Db 954 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 895
|||||

QY 182 TCCTCCTCATCTTCAATGCTGAGTTGACAGTGTGGTGTGCCCTGGTGATACACATAA 241
|||||
Db 894 TCCTCCTCATCTTCAATGCTGAGTTGACAGTGTGGTGTGCCCTGGTGATACACATAA 835
|||||

QY 242 TGGCTGAGCATTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
|||||
Db 834 TGGCTGAGCATTCTCGCTTGTGCTAGTGCCTGCCATCAAGAA 789
|||||

BD242023.1 GI:33051793
JP 2002520054-A/110.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1289)
AUTHORS Dillon,D.C., Harlocker,S.L., Yudiu,J., Xu,J. and Mitcham,J.L.
TITLE Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use
JOURNAL Patent: JP 2002520054-A 110 09-JUL-2002;
CORIXA CORP
COMMENT OS Homo sapiens (human)
PN JP 2002520054-A/110
PD 09-JUL-2002
PF 14-JUL-1999 JP 2000560247
PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR
09-APR-1999 US 09/288946
PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI
JIANGCHUN XU,
PI JENNIFER LYNN MITCHAM
PC C12N15/09,A61K38/00,A61K39/395,C07K14/47,C07K16/30,
PC C12N5/10,
PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
PC A61K37/02,
PC C12N5/00
CC Compounds for immunotherapy and diagnosis of prostate cancer and methods
CC for their use
FH Key Location/Qualifiers
FT source 1..1289
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..1289
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
|||||
Db 220 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 279
|||||

QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 121
|||||
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 339
|||||

QY 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
|||||
Db 340 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 399
|||||

QY 182 TCCTCCTCATCTTCAATGCTGAGTTGACAGTGTGGTGTGCCCTGGTGATACACATAA 241
|||||
Db 400 TCCTCCTCATCTTCAATGCTGAGTTGACAGTGTGGTGTGCCCTGGTGATACACATAA 459
|||||

QY 242 TGGCTGAGCATTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
|||||
Db 460 TGGCTGAGCATTCTCGCTTGTGCTAGTGCCTGCCATCAAGAA 505
|||||

RESULT 14
AR237206
LOCUS AR237206 1289 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 111 from patent US 6465611.
ACCESSION AR237206
VERSION AR237206.1 GI:27281864
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1289)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 111 15-OCT-2002;
FEATURES Location/Qualifiers
1..1289
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGGCCATGCAGT 61
DB 220 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGGCCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACCGCGCGCTTGTGGTCTTTGTGGTTTCC 121
DB 280 TTGTCAACGTGGGCTACTTCTCATCGACCGCGCGCTTGTGGTCTTTGTGGTTTCC 339
QY 122 TGGGCTGCTATGCTGTGAAGACTTGACGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
DB 340 TGGGCTGCTATGCTGTGAAGACTTGACGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 399
QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCATAA 241
DB 400 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCATAA 459
QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 460 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 505
RESULT 15
AR278230
LOCUS AR278230 1289 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 111 from patent US 6512094.
ACCESSION AR278230
VERSION AR278230.1 GI:29712476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1289)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 111 28-JAN-2003;
FEATURES Location/Qualifiers
1..1289
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGGCCATGCAGT 61
DB 220 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGGCCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACCGCGCGCTTGTGGTCTTTGTGGTTTCC 121

DB 280 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTTGTGGTCTTTGTCTTTGGTTTCC 339
QY 122 TGGGCTGCTATGCTGTGAAGACTTGACGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
DB 340 TGGGCTGCTATGCTGTGAAGACTTGACGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 399
QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCATAA 241
DB 400 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCATAA 459
QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 460 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 505
Search completed: August 27, 2005, 09:49:23
Job time : 1580.61 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August: 27, 2005, 08:08:44 ; Search time 2770.4 Seconds
(without alignments)
4080.665 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatgggcatcctt.....ccatcaagaagattatgggt 297

Scoring table: IDENTITY NUC

Gap 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283.2	95.4	777	7	CF595432
2	282.8	95.2	518	6	CB161656 K-EST0221
3	282.8	95.2	539	6	CD709223 EST25750
4	282.8	95.2	542	4	BM819747
5	282.8	95.2	543	4	BM819711
6	282.8	95.2	546	6	CD700012 EST16536
7	282.8	95.2	549	2	BE249898 600942941
8	282.8	95.2	554	4	BM819756 K-EST0087
9	282.8	95.2	559	5	EX480177 DKFZp686E
10	282.8	95.2	564	4	BG428609 602494743
11	282.8	95.2	566	4	BM819724 K-EST0087
12	282.8	95.2	568	5	BP261193 BP261193
13	282.8	95.2	568	5	BP262643 BP262643
14	282.8	95.2	571	4	BM819701 K-EST0087
15	282.8	95.2	571	5	BP262874 BP262874
16	282.8	95.2	573	5	BP263326 BP263326
17	282.8	95.2	576	5	BP260827 BP260827
18	282.8	95.2	579	6	CD701289 EST17813
19	282.8	95.2	581	5	BP254783 BP254783
20	282.8	95.2	581	5	BP262395 BP262395
21	282.8	95.2	582	5	BP260782 BP260782
22	282.8	95.2	582	5	BP261111 BP261111
23	282.8	95.2	582	5	BP263686 BP263686
24	282.8	95.2	582	5	BP263741 BP263741

ALIGNMENTS

```

RESULT 1
CF595432
LOCUS
DEFINITION
  CF595432 777 bp mRNA linear EST 26-SEP-2003
  IMAGE:30703089 5', mRNA sequence.
ACCESSION
  CF595432.1 GI:36350884
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 777)
  NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS
  National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
  Unpublished (1999)
JOURNAL
  Contact: Daniela S. Gerhard, Ph.D.
COMMENT
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Arnold Schwartz, MD, PhD
  DNA Library Preparation: CLONTECH Laboratories, Inc.
  DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDCM249. row: p column: 10
  High quality sequence stop: 453.
  Location/Qualifiers
    1..777
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:30703089"
      /tissue_type="Stomach, adenocarcinoma"
      /lab_host="DH10B (TL phage-resistant)"
      /clone_lib="NCI CGAP St"
      /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
      Site 2: SfiI (ggcgctcgcc); Library is oligo-dT primed
      and directionally cloned. 5' and 3' adaptors were used in
      cloning as follows: 5' adaptor sequence:
      5'-CAGGCCCATATGGCC-3' and 3' adaptor sequence:
      5'-ATTGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
      C, or G and N = A, C, G, or T). Average insert size 1.30
      kb (range 0.60-3.5 kb). 15/15 colonies contained inserts

```

```

25 282.8 95.2 582 5 BP276804
26 282.8 95.2 582 5 BP330600
27 282.8 95.2 582 5 BP330653
28 282.8 95.2 582 5 BP330738
29 282.8 95.2 582 5 BP330807
30 282.8 95.2 582 6 CD698393
31 282.8 95.2 583 4 BM819683
32 282.8 95.2 583 5 BP255135
33 282.8 95.2 583 5 BP260638
34 282.8 95.2 583 5 BP262132
35 282.8 95.2 583 5 BP342136
36 282.8 95.2 584 5 BP263144
37 282.8 95.2 585 5 BP331321
38 282.8 95.2 585 6 CB216655
39 282.8 95.2 586 4 BM836692
40 282.8 95.2 601 4 BM819685
41 282.8 95.2 604 6 CD704563
42 282.8 95.2 610 6 CD699899
43 282.8 95.2 613 4 BM828457
44 282.8 95.2 614 6 CD691226
45 282.8 95.2 622 6 CD698114

```

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN	Query Match Best Local Similarity Matches	95.4%; 99.0%; 285;	Score 283.2; Pred. No. 2.6e-68; 0;	DB 7; Length 777; 0;	Indels 3;	Gaps 0;
Qy	2	CAATCGAATGGGCATCCCTTCTGAAGATCTTTCGGGCCACTGTCGTCAGTGCCCATGCA	61			
Db	241	CAATCGATGGGCATCCCTTCTGAAGATCTTTCGGGCCACTGTCGTCAGTGCCCATGCA	300			
Qy	62	TTGTCAACGTCGGCTACTTCTCTCATCCGACGCGCGGTGTGGTCTTTGGTCTTGGTTTCC	121			
Db	301	TTGTCAACGTCGGCTACTTCTCTCATCCGACGCGCGGTGTGGTCTTTGGTCTTGGTTTCC	360			
Qy	122	TGGGCTGCTATGGTGCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	181			
Db	361	TGGGCTGCTATGGTGCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	420			
Qy	182	TCCTTCCTCATCTTCATTGCTCAGGTTGCAGCTGCTGTGGTGCCTTGGTGACACCAATAA	241			
Db	421	TCCTTCCTCATCTTCATTGCTCAGGTTGCAGCTGCTGTGGTGCCTTGGTGACACCAATAA	480			
Qy	242	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCATCAAGAAGA	289			
Db	481	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCATCAAGAAGA	528			

RESULT 2	
CB161656	
LOCUS	518 bp mRNA linear EST 30-JAN-2003
DEFINITION	K-EST0221639 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-48-D07
ACCESSION	CB161656
VERSION	CB161656
KEYWORDS	5', mRNA sequence.
SOURCE	CB161656.1 GI:28147782
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 518)
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

```

FEATURES
  source
    nrgn query sequence stop: 518.
    Location/Qualifiers
      1. 518
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="Li8POOLIn1-48-D07"
        /cell_line="GNU-354+Cho-CK+Choi-CK+HLK-3"
        /lab_host="Top10P"
        /clone_lib="Li8POOLIn1"
        /note="Organ: Liver; Vector: pT73-Pac; Site 1: ECORI;
        Site 2: NotI; The library was contributed by the Soares
        laboratory and it was constructed as described by Bonaldo,
        M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
        6(9): 791-806. RNA was prepared from harvested cell
        culture."
ORIGIN

```

Query Match	95.2%	Score 282.8	DB 6	Length 518
Best Local Similarity	99.3%	Pred. No. 3.1e-68		
Matches 284	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	2	CAATCGATGGGCATCTTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCCATGCAGT	61	
Db	225	CAATCGATGGGCATCTTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCCATGCAGT	284	
QY	62	TTGTCAACGTGGGCTACTTCTCATCGACCGCGGCTTGTGGTCTTTGGCTCTTGGTTTCC	121	
Db	285	TTGTCAACGTGGGCTACTTCTCATCGACCGCGGCTTGTGGTCTTTGGCTCTTGGTTTCC	344	
QY	122	TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGACGGTCTTCTTCATCC	181	
Db	345	TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGACGGTCTTCTTCATCC	404	
QY	182	TCCTCCTCATCTTCATTGCTTGAGGTTTCGAGCTGCTGTGGTCGCCTTGGTGACACCAATAA	241	
Db	405	TCCTCCTCATCTTCATTGCTTGAGGTTTCGAGCTGCTGTGGTCGCCTTGGTGACACCAATAA	464	
QY	242	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCTTGCCTGCCATCAAGAA	287	
Db	465	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCTTGCCTGCCATCAAGAA	510	
RESULT 3				
CD709223				
LOCUS	CD709223	539 bp	mRNA	linear
DEFINITION	EST25750	human nasopharynx	Homo sapiens	cdNA, mRNA sequence.
ACCESSION	CD709223			
VERSION	CD709223.1	GI:32239853		
KEYWORDS	EST.			

CD709223	539 bp	mrna	linear	EST 25-JUN-2000
EST25750	human nasopharynx	Homo sapiens	cDNA, mRNA sequence.	
CD709223				
CD709223.1	GI:322239853			
EST.				
Source	Homo sapiens (human)			
Organism	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
Reference	1 (bases 1 to 539)			
Authors	Zhu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Leng, Y.-X.			
Title	Transcriptional Gene Expression Profile of Human Nasopharynx			
Journal	Unpublished (2003)			
Comment	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: vxzeng@zszums.edu.cn.			

```

source
1. .539
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match          95.2%;   Score 282.8;   DB 6;   Length 539;
Best Local Similarity 99.3%;   Pred. No. 3.1e-68;
Matches 284;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0

Qy  2  CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGCTCGTCCAGTCCCATGCAGT 61
Db  156 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGCTCGTCCAGTCCCATGCAGT 215

Qy  62  TTGTCAACGTGGGTACTTCTCATCGACGCCGGTTGGTCTTTGGTCTTTGGTTTCC 121
Db  216 TTGTCAACGTGGGTACTTCTCATCGACGCCGGTTGGTCTTTGGTCTTTGGTTTCC 275

Qy  122 TGGGCTGCTATGGTGCTAAAGACTGAGAGCAAGTGTGCCTCGTGACGTTCTTCTTTCATCC 181

```

```

Db      276  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTCTTCTTCATCC 335
Qy      182  TCTCTCCTCATCTTCATCTGCTGAGGTGGAGCTGCTGTGTGCTGCTTGGTGTACACCAATAA 241
Db      336  TCTCTCCTCATCTTCATCTGCTGAGGTGGAGCTGCTGTGTGCTGCTTGGTGTACACCAAA 395
Qy      242  TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCTGCCATCAAGAA 287
Db      396  TGGCTGAGCACTTCTGCTGCTGTGTAGTGCTGCCATCAAGAA 441

RESULT 4
BM819747
LOCUS   K-EST0087909 S18N669761 Homo sapiens cDNA clone S18N669761-20-G10
DEFINITION 5', mRNA sequence.
ACCESSION BM819747
VERSION   BM819747.1 GI:19176160
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE    21C Frontier Korean EST Project 2001
JOURNAL  Unpublished (2002)
COMMENT  Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: G column: 10
High quality sequence stop: 542.
Location/Qualifiers
1..542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-G10"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 542;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
Db      206  CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 265

```

```

Qy      62  TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTCC 121
Db      266  TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTCC 325
Qy      122  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db      326  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 385
Qy      182  TCCTCCTCATCTTCATCTGCTGAGGTGGAGCTGCTGTGTGCTGCCCTGGTGTACACCAATAA 241
Db      386  TCCTCCTCATCTTCATCTGCTGAGGTGGAGCTGCTGTGTGCTGCCCTGGTGTACACCAAA 445

Qy      242  TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCTGCCATCAAGAA 287
Db      446  TGGCTGAGCACTTCTGCTGCTGTAGTGCTGCCATCAAGAA 491

RESULT 5
BM819711
LOCUS   K-EST0087869 S18N669761 Homo sapiens cDNA clone S18N669761-20-D06
DEFINITION 5', mRNA sequence.
ACCESSION BM819711
VERSION   BM819711.1 GI:19176124
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE    21C Frontier Korean EST Project 2001
JOURNAL  Unpublished (2002)
COMMENT  Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: D column: 06
High quality sequence stop: 543.
Location/Qualifiers
1..543
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-D06"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 543;

```

```
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db |||
QY 246 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 305
Db |||
QY 62 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 121
Db |||
QY 306 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 365
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db |||
QY 366 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 425
Db |||
QY 182 TCCTCCTCATCTTCATTTGCTGAGTGTGACGTCGTCGTGGTGCCTTGGTGTACACCAATA 241
Db |||
QY 426 TCCTCCTCATCTTCATTTGCTGAGTGTGACGTCGTCGTGGTGCCTTGGTGTACACCAATA 485
Db |||
QY 242 TGGCTGAGCACTTCCTCGAGCTTGCCTGTAGTGCCTGCCATCAAGAA 287
Db |||
QY 486 TGGCTGAGCACTTCCTCGAGCTTGCCTGTAGTGCCTGCCATCAAGAA 531
Db |||

RESULT 6
CD700012 546 bp mRNA linear EST 25-JUN-2003
LOCUS EST16536 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD700012
ACCESSION CD700012
VERSION CD700012.1 GI:32229841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
source
1. 546
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 546;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db |||
QY 255 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 314
Db |||
QY 62 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 121
Db |||
QY 315 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 374
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db |||
QY 375 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 434
Db |||
```

```
QY 182 TCCTCCTCATCTTCATTTGCTGAGTGTGACGTCGTCGTGGTGCCTTGGTGTACACCAATA 241
Db |||
QY 435 TCCTCCTCATCTTCATTTGCTGAGTGTGACGTCGTCGTGGTGCCTTGGTGTACACCAATA 494
Db |||
QY 242 TGGCTGAGCACTTCCTCGAGCTTGCCTGTAGTGCCTGCCATCAAGAA 287
Db |||
QY 495 TGGCTGAGCACTTCCTCGAGCTTGCCTGTAGTGCCTGCCATCAAGAA 540
Db |||

RESULT 7
BE249898 549 bp mRNA linear EST 13-JUL-2000
LOCUS 60942941P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959379 5',
DEFINITION mRNA sequence.
ACCESSION BE249898
VERSION BE249898.1 GI:9120001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM51 row: a column: 12
High quality sequence stop: 549.

FEATURES
source
1. 549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2959379"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/notes="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 95.2%; Score 282.8; DB 2; Length 549;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db |||
QY 206 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 265
Db |||
QY 62 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 121
Db |||
QY 266 TTGTCAAGCTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTCCTCTTGGTTTCC 325
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db |||
QY 326 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 385
Db |||
QY 182 TCCTCCTCATCTTCATTTGCTGAGTGTGACGTCGTCGTGGTGCCTTGGTGTACACCAATA 241
Db |||
```

```

Db      386 TCCTCTCATCTTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTTGGTGTATACACCACAA 445
QY      242 TGCGTGAAGCACTTCCGACGTTCTGCTAGTCTGCTGCATCAAGAA 287
      |||||
Db      446 TGCGTGAAGCACTTCCCTGACGTTCTGCTAGTCTGCTGCATCAAGAA 491
      |||||

RESULT 8
BM819756      554 bp mRNA linear EST 06-MAR-2002
LOCUS      K-EST0087919 S18N669761 Homo sapiens cDNA clone S18N669761-20-H08
DEFINITION      5', mRNA sequence.
ACCESSION      BM819756
VERSION      BM819756.1 GI:19176169
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 554)
AUTHORS      Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
      Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
      Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL      Unpublished (2002)
COMMENT      Contact: Kim YS
      Genome Research Center
      Korea Research Institute of Bioscience & Biotechnology
      52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
      Tel: +82-42-860-4470
      Fax: +82-42-860-4409
      Email: yongsung@mail.kribb.re.kr
      Plate: 20 row: H column: 08
      High quality sequence stop: 554.
      Location/Qualifiers
FEATURES      source
      1..554
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="S18N669761-20-H08"
      /sex="F"
      /lab_host="Top10F"
      /clone_lib="S18N669761"
      /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
      Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
      bacterial alkaline phosphatase (BAP) and then decapped
      with tobacco acid pyrophosphatase (TAP). The decapped
      intact mRNA was ligated with DNA-RNA linker including EcoR
      I site by treatment of T4 RNA ligase and the first strand
      cDNA was synthesized from oligo dT-selected mRNA by
      priming with dT-tailed vector. The dT-tailed vector was
      adjusted to have about 60nt. The cDNA vector was
      circularized with E. coli DNA ligase after digestion of
      EcoRI which site is also included in vector. An RNA strand
      converted to a DNA strand by Okayama-Berg method. The
      obtained cDNA vectors were used for transformation of
      competent cells E. coli Top10F by electroporation method.
      The cDNA libraries constructed by this method are
      full-length enriched cDNA library."

ORIGIN
Query Match      95.2%; Score 282.8; DB 4; Length 554;
Best Local Similarity      99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 61
Db      231 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 290
QY      62 TTGTCACAGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 121
Db      291 TTGTCACAGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 350

```

```

QY      122 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTTCTTTTCATCC 181
Db      351 TGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTTCTTTTCATCC 410
QY      182 TCCTCTCATCTTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACATAA 241
Db      411 TCCTCTCATCTTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACACAA 470
QY      242 TGGCTGAGCACATCCCGAGCTTCTGCTAGTGCCTGCCATCAAGAA 287
Db      471 TGGCTGAGCACATCTCTGAGCTTCTGCTAGTGCCTGCCATCAAGAA 516

RESULT 9
BX480177      559 bp mRNA linear EST 04-SEP-2003
LOCUS      DKFP686E20218_r1 686 (synonym: hlccc3) Homo sapiens cDNA clone
DEFINITION      DKFP686E20218 5', mRNA sequence.
ACCESSION      BX480177
VERSION      BX480177.1 GI:31916638
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 559)
AUTHORS      Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
      Fobo,G., Han,M. and Wiemann,S.
TITLE      EST (Bioecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL      Unpublished (2003)
COMMENT      Contact: MIPS
      MIPS
      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
      This is the 5' sequence of the clone insert
      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
      Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
      sequenced by GBF (National Research Centre for Biotechnology Ltd.,
      Braunschweig/Germany) within the cDNA sequencing consortium of the
      German Genome Project.
      No sl sequence available.
      This clone (DKFP686E20218) is available at the RZPD in Berlin.
      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
      Location/Qualifiers
FEATURES      source
      1..559
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="DKFP686E20218"
      /dev_stage="adult"
      /lab_host="DH10B"
      /clone_lib="686 (synonym: hlccc3)"
      /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
      cDNA-collection"

ORIGIN
Query Match      95.2%; Score 282.8; DB 5; Length 559;
Best Local Similarity      99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 61
Db      234 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 293
QY      62 TTGTCACAGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTGCTTTGTTTCC 121
Db      294 TTGTCACAGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTGCTTTGTTTCC 353
QY      122 TGGGCTGCTATGGTCTAAGACTGAGACAGTGTGCCCTCGTGAGCTTCTTTTCATCC 181
Db      354 TGGGCTGCTATGGTCTAAGACTGAGACAGTGTGCCCTCGTGAGCTTCTTTTCATCC 413
QY      182 TCCTCTCATCTTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACATAA 241

```

Db 414 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGATACACCACA 473
QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 474 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 519

RESULT 10
LOCUS BG428609 564 bp mRNA linear EST 14-MAR-2001
DEFINITION 602494743F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608394 5', mRNA sequence.
ACCESSION BG428609
VERSION BG428609.1 GI:13335115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 564)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Placer: LLM1350 row: f column: 11
High quality sequence stop: 560.
Location/Qualifiers
1..564
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608394"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccggccg); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

FEATURES
source
1..564
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608394"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccggccg); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 564;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
Db 233 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 292
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTGGTTTCC 121
Db 293 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTGGTTTCC 352
QY 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 353 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 412
QY 182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGATACACCAPAA 241

Db 413 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGATACACCACA 472
QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db 473 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 518

RESULT 11
LOCUS BM819724 566 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0087883 S18N669761 Homo sapiens cDNA clone S18N669761-20-E08 5', mRNA sequence.
ACCESSION BM819724
VERSION BM819724.1 GI:19176137
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: vongseung@mail.kribb.re.kr
Plate: 20 row: E column: 08
High quality sequence stop: 566.
Location/Qualifiers
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-E08"
/sex="F"
/lab_host="Top10P"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

FEATURES
source
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-E08"
/sex="F"
/lab_host="Top10P"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 566;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
Db 232 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 291
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTGGTTTCC 121
Db 292 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTGGTTTCC 351

QY 122 TGCGCTGCTATGCTGAAGCACTGAGACCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 181
 Db 352 TGCGCTGCTATGCTGAAGCACTGAGACCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 411

QY 182 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 241
 Db 412 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 471

QY 242 TGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 287
 Db 472 TGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 517

RESULT 12
 BP261193
 LOCUS BP261193 568 bp mRNA linear EST 16-SEP-2004
 DEFINITION BP261193 Sugano cDNA library, small intestine Homo sapiens cDNA
 clone HSI02743, mRNA sequence.
 ACCESSION BP261193
 VERSION BP261193.1 GI:52176424
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 568)
 Sasaki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HSI02743"
 /tissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
 Query Match 95.2%; Score 282.8; DB 5; Length 568;
 Best Local Similarity 99.3%; Pred. No. 3.1e-68;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 Db 238 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 297

QY 62 TTGTCAACGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 121
 Db 298 TTGTCAACGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 357

QY 122 TGGGCTGCTATGCTGAAGCACTGAGCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 181
 Db 358 TGGGCTGCTATGCTGAAGCACTGAGCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 417

QY 182 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 241
 Db 418 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 477

QY 242 TGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 287
 Db 478 TGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 523

RESULT 13
 BP262643

LOCUS BP262643 568 bp mRNA linear EST 16-SEP-2004
 DEFINITION BP262643 Sugano cDNA library, small intestine Homo sapiens cDNA
 clone HSI07585, mRNA sequence.
 ACCESSION BP262643
 VERSION BP262643.1 GI:52177874
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 568)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HSI07585"
 /tissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
 Query Match 95.2%; Score 282.8; DB 5; Length 568;
 Best Local Similarity 99.3%; Pred. No. 3.1e-68;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 Db 233 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 292

QY 62 TTGTCAACGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 121
 Db 293 TTGTCAACGTGGGCTACTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 352

QY 122 TGGGCTGCTATGCTGAAGCACTGAGCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 181
 Db 353 TGGGCTGCTATGCTGAAGCACTGAGCAAGTGTGCCCTCGTGAAGTCTTCTTTCATCC 412

QY 182 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 241
 Db 413 TCCTCTCATCTTCATGCTGAGGTTCAGCTGCTGTGGTGGCTTGGTGTACACATCA 472

QY 242 TGGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 287
 Db 473 TGGCTGAGCACTTCCCGAGCTTCTGCTAGTGTGCTGCCATCAAGAA 518

RESULT 14
 BP2619701
 LOCUS BP2619701 571 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0087855 S18N669761 Homo sapiens cDNA clone S18N669761-20-C03
 5', mRNA sequence.
 ACCESSION BP2619701
 VERSION BP2619701.1 GI:19176114
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 571)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL
COMMENT

Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: C column: 03
High quality sequence scop: 571.
Location/Qualifiers
1. 571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-C03"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

FEATURES
source

1. 571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-20-C03"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 4; Length 571;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 237 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 296

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTTTGCTTTCC 121
DB 297 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTTTGCTTTCC 356

QY 122 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 181
DB 357 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 416

QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGACAGTGCCTCGTGCAGTTCCTTCTTCATCC 241
DB 417 TCCTCCTCATCTTCATTTGCTGAGGTTGACAGTGCCTCGTGCAGTTCCTTCTTCATCC 476

QY 242 TGGCTGAGCATTCCCGACGTTGCTGTTAGTGCCTGCGCATCAAGAA 287
DB 477 TGGCTGAGCATTCCCTGAGCTTGCTGGTAGTGCCTGCGCATCAAGAA 522

RESULT 15
BP262874

LOCUS BP262874 Sugano cDNA library, 571 bp mRNA linear EST 16-SEP-2004
DEFINITION clone HS108372, mRNA sequence.
ACCESSION BP262874
VERSION BP262874.1 GI:52178105
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 571)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1. 571

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS108372"

/tissue type="small intestine"

/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Query Match 95.2%; Score 282.8; DB 5; Length 571;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 233 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 292

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTTTCC 121
DB 293 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTTTCC 352

QY 122 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 181
DB 353 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 412

QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGACAGTGCCTCGTGCAGTTCCTTCTTCATCC 241
DB 413 TCCTCCTCATCTTCATTTGCTGAGGTTGACAGTGCCTCGTGCAGTTCCTTCTTCATCC 472

QY 242 TGGCTGAGCATTCCCGACGTTGCTGGTAGTGCCTGCGCATCAAGAA 287
DB 473 TGGCTGAGCATTCCCTGAGCTTGCTGGTAGTGCCTGCGCATCAAGAA 518

Search completed: August 27, 2005, 11:16:20
Job time : 2773.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:38:03 ; Search time 545.032 Seconds
(without alignments)
3565.473 Million cell updates/sec

Title: US-10-079-954-1
Perfect score: 297
Sequence: 1 gcaatcgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues
Total number of hits satisfying chosen parameters: 14663456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
 - 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	13	US-10-079-954-1
2	282.8	95.2	513	14	Sequence 1, Appli
3	282.8	95.2	635	9	Sequence 203, App
c	282.8	95.2	635	9	Sequence 1025, Ap
c	282.8	95.2	635	13	Sequence 1025, Ap
6	282.8	95.2	792	9	Sequence 1025, Ap
7	282.8	95.2	1044	19	Sequence 361, App
					Sequence 132, App

8	282.8	95.2	1076	14	US-10-097-340-325	Sequence 325, App
9	282.8	95.2	1076	15	US-10-205-823-424	Sequence 424, App
10	282.8	95.2	1076	17	US-10-172-118-1191	Sequence 1191, Ap
11	282.8	95.2	1076	18	US-10-342-887-1191	Sequence 1191, Ap
12	282.8	95.2	1076	19	US-10-775-920-136	Sequence 136, App
13	282.8	95.2	1154	14	US-10-097-340-323	Sequence 323, App
14	282.8	95.2	1154	15	US-10-205-823-422	Sequence 422, App
15	282.8	95.2	1278	17	US-10-295-027-603	Sequence 603, App
16	282.8	95.2	1278	18	US-10-420-425-400	Sequence 400, App
17	282.8	95.2	1278	19	US-10-775-920-130	Sequence 130, App
18	282.8	95.2	1288	15	US-10-156-136-4	Sequence 4, Appli
19	282.8	95.2	1288	15	US-10-156-136-50	Sequence 50, Appli
20	282.8	95.2	1288	24	US-11-041-419-4	Sequence 4, Appli
c	282.8	95.2	1288	24	US-11-041-419-50	Sequence 50, Appli
22	282.8	95.2	1289	9	US-09-759-143-111	Sequence 111, App
23	282.8	95.2	1289	9	US-09-780-669-111	Sequence 111, App
24	282.8	95.2	1289	9	US-09-030-606-111	Sequence 111, App
25	282.8	95.2	1289	9	US-09-822-827-111	Sequence 111, App
26	282.8	95.2	1289	9	US-09-115-453-111	Sequence 111, App
27	282.8	95.2	1289	9	US-09-232-880-111	Sequence 111, App
28	282.8	95.2	1289	9	US-09-895-793-111	Sequence 111, App
29	282.8	95.2	1289	9	US-09-895-814-111	Sequence 111, App
30	282.8	95.2	1289	13	US-10-012-896-111	Sequence 111, App
31	282.8	95.2	1289	14	US-10-010-940-111	Sequence 111, App
32	282.8	95.2	1289	16	US-10-144-678A-111	Sequence 111, App
33	282.8	95.2	1289	16	US-10-294-025-111	Sequence 111, App
34	282.8	95.2	1289	19	US-10-688-838-111	Sequence 111, App
35	282.8	95.2	1297	19	US-10-775-920-131	Sequence 131, App
36	282.8	95.2	1297	19	US-10-775-920-133	Sequence 133, App
37	282.8	95.2	1306	19	US-10-775-920-134	Sequence 134, App
38	282.8	95.2	1324	10	US-09-981-876-82	Sequence 82, Appl
39	282.8	95.2	1324	10	US-09-148-545-82	Sequence 82, Appl
40	282.8	95.2	1376	9	US-09-981-876-14	Sequence 14, Appl
41	282.8	95.2	1376	10	US-09-148-545-14	Sequence 14, Appl
42	282.8	95.2	1456	9	US-09-981-353-133	Sequence 133, App
43	282.8	95.2	1533	21	US-10-918-897-14	Sequence 14, Appl
44	282.8	95.2	1603	10	US-09-814-353-21202	Sequence 21202, A
45	282.8	95.2	1603	20	US-10-357-930-23347	Sequence 23347, A

ALIGNMENTS

RESULT 1
US-10-079-954-1
; Sequence 1, Application US/10079954
; Publication No. US2002016861A1
; GENERAL INFORMATION:
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09302857)
; CURRENT APPLICATION NUMBER: US/10/079,954
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US/09/308,984
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-954-1

Query Match 100.0%; Score 297; DB 13; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAATCGATGGGCGCATCCTTTCTGAAGATCTTCGGGCGCACTGTCTCCAGTCCCATGCG 60
|||||


```
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(635)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-1025

Query Match          95.2%; Score 282.8; DB 9; Length 635;
Best Local Similarity 99.3%; Pred. No. 5.4e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db |||||||
575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 516
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 121
Db |||||||
515 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 456
QY 122 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 181
Db |||||||
455 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 396
QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 241
Db |||||||
395 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 336
QY 242 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 287
Db |||||||
335 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 290

RESULT 6
US-09-878-134-361
; Sequence 361, Application US/09878134
; Publication No. US20020086303A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.532
; CURRENT APPLICATION NUMBER: US/09/878,134
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 361
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-878-134-361

Query Match          95.2%; Score 282.8; DB 9; Length 792;
Best Local Similarity 99.3%; Pred. No. 5.8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db |||||||
214 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 273
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 121
Db |||||||
274 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 333
QY 122 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 181
Db |||||||
334 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 393
QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 241
Db |||||||
394 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 453
QY 242 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 287
Db |||||||
454 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 499

RESULT 7
US-10-775-920-132
; Sequence 132, Application US/10775920
; Publication No. US2004017544A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1025

Query Match          95.2%; Score 282.8; DB 13; Length 635;
Best Local Similarity 99.3%; Pred. No. 5.4e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db |||||||
575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 516
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 121
Db |||||||
515 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGTCTTTGTCTTTGTTTCC 456
QY 122 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 181
Db |||||||
455 TGGGCTGCTATGCTGCTTAAGACTGAGAGCAAGTGTGCTCGTGTGAGCTTCTTTCATCC 396
QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 241
Db |||||||
395 TCCTCCTCATCTTCATTCCTGAGGTTGAGCTGCTGTGTGCTCGCTTGTGTACACCATAA 336
QY 242 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 287
Db |||||||
335 TGGCTGAGCACTTCCGAGCTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 290

RESULT 5
US-10-025-380-1025/c
; Sequence 1025, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugui
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yaseir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1025
```

```
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Meigen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-132

Query Match          95.2%; Score 282.8; DB 19; Length 1044;
Best Local Similarity 99.3%; Pred. No. 6.2e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGAGT 61
DB 221 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGAGT 280
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGCTCTTGGTTTCC 121
DB 281 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGCTCTTGGTTTCC 340
QY 122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 341 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 400
QY 182 TCCTCCTCATCTTCAATTCGTAGGTTGACGCTGCTGTGGTGCCCTTGGTGACACCAATA 241
DB 401 TCCTCCTCATCTTCAATTCGTAGGTTGACGCTGCTGTGGTGCCCTTGGTGACACCAATA 460
QY 242 TGGCTGAGCAGTTCCTCCGACGTTGCTGCTAGTGCCCTGCGCCATCAAGAA 287
DB 461 TGGCTGAGCAGTTCCTCCGACGTTGCTGCTAGTGCCCTGCGCCATCAAGAA 506

RESULT 8
US-10-097-340-325
; Sequence 325, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Katen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
```

```
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-325

Query Match          95.2%; Score 282.8; DB 14; Length 1076;
Best Local Similarity 99.3%; Pred. No. 6.3e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGAGT 61
DB 98 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGAGT 157
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGCTCTTGGTTTCC 121
DB 158 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGCTCTTGGTTTCC 217
QY 122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCAATTCGTAGGTTGACGCTGCTGTGGTGCCCTTGGTGACACCAATA 241
DB 278 TCCTCCTCATCTTCAATTCGTAGGTTGACGCTGCTGTGGTGCCCTTGGTGACACCAATA 337
QY 242 TGGCTGAGCAGTTCCTCCGACGTTGCTGCTAGTGCCCTGCGCCATCAAGAA 287
DB 338 TGGCTGAGCAGTTCCTCCGACGTTGCTGCTAGTGCCCTGCGCCATCAAGAA 383

RESULT 9
US-10-205-823-424
; Sequence 424, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
```

```
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-424

Query Match
Best Local Similarity 95.2%; Score 282.8; DB 15; Length 1076;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 61
DB 98 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 157

QY 62 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 121
DB 158 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 217

QY 122 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 277

QY 182 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 241
DB 278 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 337

QY 242 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 383

RESULT 10
US-10-172-118-1191
; Sequence 1191, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1191
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-118-1191

Query Match
Best Local Similarity 95.2%; Score 282.8; DB 17; Length 1076;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 61
DB 98 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 157

QY 62 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 121
DB 158 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 217

QY 122 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 277

QY 182 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 241
DB 278 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 337

QY 242 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 383

RESULT 11
US-10-342-887-1191
; Sequence 1191, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1191
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1191

Query Match
Best Local Similarity 95.2%; Score 282.8; DB 18; Length 1076;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 61
DB 98 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT 157

QY 62 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 121
DB 158 TTGTCAACGTGGGCTACTTCTTCATCGCAGCGGGGCTGTGCTTGTGCTTCTTGTTC 217

QY 122 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTAAAGACTGAGACAAAGTGTGCCCTCGTGCAGTTCCTTCATCC 277

QY 182 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 241
DB 278 TCCTCTCATCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 337

QY 242 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCGACGTTGCTGTGAGTGCCTGCTGCATCAAGAA 383

RESULT 12
US-10-775-920-136
; Sequence 136, Application US/10775920
```

```
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Merigen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-136

Query Match          95.2%; Score 282.8; DB 19; Length 1076;
Best Local Similarity 99.3%; Pred. No. 6.3e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAAGT 61
DB  98 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAAGT 157

QY  62 TTGTCACAGTGGGCGATCTTCCTCATCGCAGCGCGGTTGTGTGCTTTGCTTTGTTTCC 121
DB  158 TTGTCACAGTGGGCGATCTTCCTCATCGCAGCGCGGTTGTGTGCTTTGCTTTGTTTCC 217

QY  122 TGGGCTGCTATGCTGCTAAGACTGAGACAAGTGGCCCTCGTGAGCTTCTTCTTCATCC 181
DB  218 TGGGCTGCTATGCTGCTAAGACTGAGACAAGTGGCCCTCGTGAGCTTCTTCTTCATCC 277

QY  182 TCCTCCTCATCTTCAATTCGTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGATACACATAA 241
DB  278 TCCTCCTCATCTTCAATTCGTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGATACACATAA 337

QY  242 TGGCTGAGCACTTCGGAGCTTGTGGTAGTGCCCTGCCATCAAGAA 287
DB  338 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCCTGCCATCAAGAA 383

RESULT 13
US-10-097-340-323
; Sequence 323, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATIS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHWANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
```

```
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-323

Query Match          95.2%; Score 282.8; DB 14; Length 1154;
Best Local Similarity 99.3%; Pred. No. 6.4e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAAGT 61
DB  221 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAAGT 280

QY  62 TTGTCACAGTGGGCGATCTTCCTCATCGCAGCGCGGTTGTGTGCTTTGCTTTGTTTCC 121
DB  281 TTGTCACAGTGGGCGATCTTCCTCATCGCAGCGCGGTTGTGTGCTTTGCTTTGTTTCC 340

QY  122 TGGGCTGCTATGCTGCTAAGACTGAGACAAGTGGCCCTCGTGAGCTTCTTCTTCATCC 181
DB  341 TGGGCTGCTATGCTGCTAAGACTGAGACAAGTGGCCCTCGTGAGCTTCTTCTTCATCC 400

QY  182 TCCTCCTCATCTTCAATTCGTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGATACACATAA 241
DB  401 TCCTCCTCATCTTCAATTCGTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGATACACATAA 460

QY  242 TGGCTGAGCACTTCGGAGCTTGTGGTAGTGCCCTGCCATCAAGAA 287
DB  461 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCCTGCCATCAAGAA 506

RESULT 14
US-10-205-823-422
; Sequence 422, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wansley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
```

; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: 60/362,158
 ; PRIOR FILING DATE: 2002-03-05
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 422
 ; LENGTH: 1154
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-205-823-422

Query Match 95.2%; Score 282.8; DB 15; Length 1154;
 Best Local Similarity 99.3%; Pred. No. 6.4e-80;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 Db 221 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 280
 QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGTCTTTGTCTTTGGTTTCC 121
 Db 281 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGTCTTTGTCTTTGGTTTCC 340
 QY 122 TGGGCTGCTATGGTCTAAGACTTGAGCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 181
 Db 341 TGGGCTGCTATGGTCTAAGACTTGAGCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 400
 QY 182 TCCTCTCATCTTCATCTGCTAGGTGTCAGCTGCTGTGTGTCGCTTGGTGTCACACATAA 241
 Db 401 TCCTCTCATCTTCATCTGCTAGGTGTCAGCTGCTGTGTGTCGCTTGGTGTCACACATAA 460
 QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
 Db 461 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 506

RESULT 15

US-10-295-027-603
 ; Sequence 603, Application US/10295027
 ; Publication No. US20030232350A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 ; FILE REFERENCE: 018501-012500US
 ; CURRENT APPLICATION NUMBER: US/10/295,027
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,733
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 603
 ; LENGTH: 1278
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-295-027-603

Query Match 95.2%; Score 282.8; DB 17; Length 1278;
 Best Local Similarity 99.3%; Pred. No. 6.6e-80;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 Db 219 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 278
 QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGTCTTTGTCTTTGGTTTCC 121
 Db 279 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTTGTGTCTTTGTCTTTGGTTTCC 338
 QY 122 TGGGCTGCTATGGTCTAAGACTTGAGCAAGTGTGCCCTCGTGACGTTCTTTCATCC 181
 Db 339 TGGGCTGCTATGGTCTAAGACTTGAGCAAGTGTGCCCTCGTGACGTTCTTTCATCC 398
 QY 182 TCCTCTCATCTTCATCTGCTAGGTGTCAGCTGCTGTGTGTCGCTTGGTGTCACACATAA 241
 Db 399 TCCTCTCATCTTCATCTGCTAGGTGTCAGCTGCTGTGTGTCGCTTGGTGTCACACATAA 458
 QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
 Db 459 TGGCTGAGCACTTCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 504

Search completed: August 27, 2005, 11:33:34
 Job time : 546.032 secs

THIS PAGE BLANK (USPTO)

Result No.	Query	Score	Match	Length	DB	ID	Description	
1		256.2	98.2	261	6	A91803	Sequence 2	
2		256.2	98.2	261	6	BD023237	DNA for e	
3		247.8	94.9	421	6	CQ728213	Sequence 1	
4		247.8	94.9	1026	6	AB4653	Sequence 1	
5		247.8	94.9	1373	9	BC001291	Homo sapi	
6		247.8	94.9	1028	9	HSJ001348	Homo sapi	
7		125.6	48.1	2724	9	AK092545	Homo sapi	
8		124.4	47.7	100079	9	AC108002	Homo sapi	
9		124.4	47.7	105156	2	AF235094	Homo sapi	
10		124.4	47.7	153005	2	AC011976	Homo sapi	
11		124.4	47.7	157839	2	AC015718	Homo sapi	
12		124.4	47.7	203375	9	AC083841	Homo sapi	
13		121.2	46.4	103247	2	AF176678	Homo sapi	
14		105	40.2	201	11	BV203566	Homo sapi	
15		37.2	14.3	643	10	BC049723	Mus musc	
16		36.4	13.9	228208	2	AC119786	Rattus no	
17		36.4	13.9	262875	2	AC120775	Rattus no	
18		36.2	13.9	216132	2	AC151012	Callithri	
19		35.6	13.6	399	6	AR414779	Sequence	

/note="unnamed protein product; protein sequence is in
conflict with the conceptual translation"
/codon_start=1
/protein_id="CB69340.1"
/db_xref="GI:673355"

/translation="MALLALLLVVALPRVWTDANLTAQRDPDQRTDGDNRVWCH
VCEENTPFCQPRCKWTEPYCVIAAVKIFPRFVMAKQCSAGCAAMERPKPEKRF
LLEEPMPFFYLKCKIRYCNLEGPPIINSVFKEYAGSMGSCGGLWLAIIALLASIAA
GLSLs"

ORIGIN

Query Match 94.9%; Score 247.8; DB 6; Length 1026;
Best Local Similarity 97.3%; Pred. No. 8.5e-69;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 62
DB 522 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 581

QY 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 122
DB 582 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 641

QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
DB 642 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 701

QY 183 GATGGAGACCCAGCCAGGAG 242
DB 702 GATGGAGACCCAGCCAGGAG 761

QY 243 TTACCTCAAGTGTGTGTA 261
DB 762 TTACCTCAAGTGTGTGTA 780

RESULT 5

BC001291 1373 bp mRNA linear PRI 04-JUN-2004
LOCUS Homo sapiens cDNA for differentially expressed Col6 gene, mRNA
DEFINITION (cDNA clone IMAGE:3457263), partial cds.

ACCESSION

BC001291

VERSION

BC001291.1 GI:12654892

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1373)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, S.I., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

PUBMED 12477932

REFERENCE

2 (bases 1 to 1373)

AUTHORS

Strausberg, R.

TITLE

JOURNAL

REMARK

COMMENT

Direct Submission
Submitted (11-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 4 Row: 1 Column: 23

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 24308142.

FEATURES

source

1..1373

/organism="Homo sapiens"

/mol_type="RNA"

/db_xref="taxon:9606"

/clone="IMAGE:3457263"

/tissue type="Cervix, carcinoma"

/clone_lib="NIH MGC_12"

/lab host="DH10B"

/note="Vector: PCMV-SPORT6"

<1..1373

/gene="LY6K"

/note="synonym: HSJ001348"

/db_xref="LocusID:54742"

<1..541

/gene="LY6K"

/codon_start=2

/product="LY6K protein"

/protein_id="AAH01291.2"

/db_xref="GI:48257149"

/db_xref="LocusID:54742"

/translation="GAPRADPWPAPLGTMTALLLVVALPRVWTDANLTAQRDPED

SDRDEGNRVWCHVCEENTPFCQPRCKWTEPYCVIAAVKIFPRFVMAKQCSAG

CAAMERPKPEKRFLEPMPFFYLKCKIRYCNLEGPPIINSVFKEYAGSMGSCG

LWLAIIALLASIAAGLSLS"

ORIGIN

Query Match 94.9%; Score 247.8; DB 9; Length 1373;
Best Local Similarity 97.3%; Pred. No. 8.5e-69;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 62
DB 136 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 195

QY 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 122
DB 196 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGGAGAGAGAAACAC 255

QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
DB 256 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 315

QY 183 GATGGAGACCCAGCCAGGAG 242
DB 316 GATGGAGACCCAGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375

QY 243 TTACCTCAAGTGTGTGTA 261
DB 376 TTACCTCAAGTGTGTGTA 394

FEATURES

source
 Location/Qualifiers
 1. .2724
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="PROST2001138"
 /tissue_type="prostate"
 /clone_lib="PROST2"
 /note="cloning vector: pME18SFL3"

ORIGIN

Query Match 48.1%; Score 125.6; DB 9; Length 2724;
 Best Local Similarity 85.4%; Pred. No. 3.1e-29;
 Matches 140; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 3 CCAGCCAAAGGAGGTCACATAGATGGTGTCTCATGCTTGTCAGAGAGAAAACAC 62
 Db 149 CCAGCCGAGGAGGAGGTCACATAGATGGTGTCTCATGCTTGTCAGAGAGAAAACAC 208
 QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATATCTGCTTATAGCGGC 122
 Db 209 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATATCTGCTTATAGCGGC 268
 QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCACAGGTGCT 166
 Db 269 CGTGAAGTATCTTCGCTCTTTGTCGGGACCAAGGCAGGT 312

RESULT 8

AC108002/c
 LOCUS
 DEFINITION Homo sapiens chromosome 8, clone CTD-2292P10, complete sequence.
 AC108002
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 100079)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Gage,D., Galagan,J., Gardyna,S.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
 Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24583
 Center clone name: 2292_P_10

 Location/Qualifiers
 1. 100079
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="CTD-2292P10"
 /clone_lib="CITDI Human BAC"
 419. 549
 /rpt_family="GA-rich"
 553. 1074
 repeat_region
 repeat_region

TITLE

JOURNAL
 REFERENCE
 AUTHORS
 Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 100079)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Gage,D., Galagan,J., Gardyna,S.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
 Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 100079)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Gage,D., Galagan,J., Gardyna,S.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
 Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (07-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 7, 2002 this sequence version replaced gi:18677523.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24583
 Center clone name: 2292_P_10

 Location/Qualifiers
 1. 100079
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="CTD-2292P10"
 /clone_lib="CITDI Human BAC"
 419. 549
 /rpt_family="GA-rich"
 553. 1074
 repeat_region
 repeat_region

```
repeat_region /rpt family="BaEV-int"
1075_..1372
/rpt family="AluY"
repeat_region /rpt family="AluY"
1373_..1486
/rpt family="BaEV-int"
1675_..2715
/rpt family="BaEV-int"
2716_..2884
/rpt family="LTR10C"
2885_..2945
/rpt family="MER41C"
2946_..3186
/rpt family="AluY"
3187_..3474
/rpt family="MER41C"
4774_..4794
/rpt family="GC rich"
5015_..5035
/rpt family="GC rich"
complement(5853_..5904)
/rpt family="L3"
complement(5911_..6378)
/rpt family="MER9"
complement(6598_..6863)
/rpt family="MER4B"
6864_..6990
/rpt family="FLAM_C"
complement(6991_..7358)
/rpt family="MER4B"
7694_..7789
/rpt family="L2"
complement(9002_..9705)
/rpt family="PRIMA41-int"
complement(10037_..10582)
/rpt family="PRIMA41-int"
complement(11007_..11143)
/rpt family="PRIMA41-int"
complement(11625_..11841)
/rpt family="LMC/D"
11842_..12129
/rpt family="AluY"
complement(12130_..12507)
/rpt family="LMC/D"
complement(12522_..12679)
/rpt family="LIMEC"
complement(12847_..13113)
/rpt family="AluJo"
complement(13114_..13721)
/rpt family="LIMEC"
13725_..13926
/rpt family="LTR50"
14036_..14299
/rpt family="LTR50"
14375_..14412
/rpt family="AT rich"
complement(14787_..15222)
/rpt family="LIMEC"
complement(15239_..15395)
/rpt family="MLT1H"
complement(15516_..15634)
/rpt family="MLT1H"
15642_..15953
/rpt family="MER1B"
complement(16178_..16264)
/rpt family="LIMEC"
complement(16265_..16564)
/rpt family="AluJb"
complement(16565_..16761)
/rpt family="LIMEC"
complement(16766_..17024)
/rpt family="AluJo"
complement(17030_..17447)
/rpt family="LIMEC"

repeat_region complement(17495_..17715)
/rpt family="AluJb"
repeat_region complement(17904_..18230)
/rpt family="AluSc"
repeat_region complement(18395_..18415)
/rpt family="LIMEC"
repeat_region complement(18416_..18788)
/rpt family="MLT1A2"
repeat_region complement(18789_..18950)
/rpt family="LIMEC"
repeat_region complement(18980_..19164)

Query Match 47.7%; Score 124.4; DB 9; Length 100079;
Best Local Similarity 95.5%; Pred. No. 8.5e-29; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 6;

QY 128 AAATATTTCACGGTTTTTCATGGTTCGCAACAGGTGCTCGCGTGGTGTGCAGCATGG 187
Db 29028 AAATATTTCACGGTTTTTCATGGTTCGCAACAGGTGCTCGCGTGGTGTGCAGCATGG 28969

QY 188 AGAGACCCAGCCAGAGAGAGAGCGTTTCTCTGGAGAGCCCATGCCCTTCTTTTACC 247
Db 28968 AGAGACCCAGCCAGAGAGAGCGTTTCTCTGGAGAGCCCATGCCCTTCTTTTACC 28909

QY 248 TCAAGTGTGTAAA 261
Db 28908 TCAAGTGTGTAAA 28895

RESULT 9
AF235094/c 105156 bp DNA linear HTG 26-JUL-2002
LOCUS Homo sapiens chromosome 8 clone CTA-391H8 map 8q24, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AF235094
VERSION AF235094.3 GI:14280185
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105156)
Schilhabel,M.B., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N.,
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,
Siddiqui,R., Taudien,S., Wen,G., Rosenthal,A. and Platzer,M.
Chromosome 8 genomic sequence
Unpublished
2 (bases 1 to 105156)
Polley,A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M.,
Menzel,U. and Rosenthal,A.
Direct Submission
Submitted (14-FEB-2000) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
On Jun 2, 2001 this sequence version replaced gi:8151811.
----- Genome Center
Center: Insitute of Molecular Biotechnology
Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
----- Project Information
Center project name: H199
Center clone name: CTA-391H8
----- Summary Statistics
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 95190 bases at least Q40
Consensus quality: 98972 bases at least Q30
Consensus quality: 101536 bases at least Q20
Quality coverage: 5,49 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
```

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 30320: contig of 30320 bp in length
 * 30321 30420: gap of unknown length
 * 30421 59704: contig of 29284 bp in length
 * 59705 59804: gap of unknown length
 * 59805 83308: contig of 23504 bp in length
 * 83309 83408: gap of unknown length
 * 83409 95522: contig of 12114 bp in length
 * 95523 95623: gap of unknown length
 * 95624 98568: contig of 2945 bp in length
 * 98569 98667: gap of unknown length
 * 98668 101380: contig of 2713 bp in length
 * 101381 101480: gap of unknown length
 * 101481 103751: contig of 2271 bp in length
 * 103752 103851: gap of unknown length
 * 103852 105156: contig of 1305 bp in length.

FEATURES

source

1. .105156
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8q24"
 /clone="CTA-391H8"

ORIGIN

Query Match 47.7%; Score 124.4; DB 2; Length 105156;
 Best Local Similarity 95.5%; Pred. No. 8 6e-29;
 Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 128 AAATATTCCAGTCTTTTCATGTTTCGCAACAGGTCTCCGCTGTTGTCAGCGATCG 187
 Db 92512 AAATATTCCAGTCTTTTCATGTTTCGCAACAGGTCTCCGCTGTTGTCAGCGATCG 92453
 QY 188 AGAGACCCAGCAGGAGGAGCGGTTTCTCTGGAAGGCCATGCCCTCTTTTACC 247
 Db 92452 AGAGACCCAGCAGGAGGAGCGGTTTCTCTGGAAGGCCATGCCCTCTTTTACC 92393
 QY 248 TCAAGTGTGTAA 261
 Db 92392 TCAAGTGTGTAA 92379

RESULT 10

AC011976

LOCUS AC011976 153005 bp DNA linear HTG 13-MAY-2001
 DEFINITION Homo sapiens clone RP11-15018, WORKING DRAFT SEQUENCE, 5 unordered pieces.

AC011976

AC011976.5 GI:11560232

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 153005)

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE Homo sapiens, clone RP11-15018

JOURNAL Unpublished

AUTHORS 2 (bases 1 to 153005)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lechoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Dec 6, 2000 this sequence version replaced gi:7341825.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3500

Center clone name: 15 O 18

----- Summary Statistics

Sequencing vector: M13; M77815; 41% of reads
 Chemistry: Dye-terminator; Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 151299 bases at least Q40
 Consensus quality: 151929 bases at least Q30
 Consensus quality: 152267 bases at least Q20
 Insert size: 133000; agarose-fp
 Insert size: 152605; sum-of-contigs
 Quality coverage: 10.5 in Q20 bases; agarose-fp
 Quality coverage: 9.2 in Q20 b.

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 59732: contig of 59732 bp in length
 * 59733 59832: gap of 100 bp
 * 59833 62883: contig of 3051 bp in length
 * 62884 62983: gap of 100 bp
 * 62984 67564: contig of 4581 bp in length
 * 67565 67664: gap of 100 bp
 * 67665 121673: contig of 54009 bp in length
 * 121674 121773: gap of 100 bp
 * 121774 153005: contig of 31232 bp in length.

FEATURES

source

1. .153005
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RP11-15018"
 /clone_lib="RPC1-11 Human Male BAC"
 1. .59732
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:left"

misc_feature

59833..62883
 /note="assembly_fragment"
 62984..67564
 /note="assembly_fragment"
 67665..121673
 /note="assembly_fragment"
 121774..153005
 /note="assembly_fragment"
 clone_end:T7
 vector_side:right"

misc_feature

59833..62883
 /note="assembly_fragment"

misc_feature

62984..67564
 /note="assembly_fragment"

misc_feature

67665..121673
 /note="assembly_fragment"

misc_feature

121774..153005
 /note="assembly_fragment"

clone_end:T7

vector_side:right"

ORIGIN

```

Query Match          47.7%; Score 124.4; DB 2; Length 153005;
Best Local Similarity 95.5%; Pred. No. 8.6e-29;
Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 AAATATTTCCAGCTTTTTCATGTTTCGCAACAGGTGCTCCGCTCGTTGTGTCAGCGATGG 187
    |||||
Db 18636 AAATATTTCCAGCTTTTTCATGTTTCGCAACAGGTGCTCCGCTCGTTGTGTCAGCGATGG 18695

QY 188 AGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTCTTTTACC 247
    |||||
Db 18696 AGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTCTTTTACC 18755

QY 248 TCAAGTGTGTGTA 261
    |||||
Db 18756 TCAAGTGTGTGTA 18769

RESULT 11
AC015718
LOCUS
DEFINITION Homo sapiens clone RP11-119A16, 4 unordered pieces.
ACCESSION AC015718
VERSION AC015718.6 GI:18642769
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157839)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome, clone RP11-119A16
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 157839)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Balwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,D., Doyle,M.,
Ferrelra,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galgán,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehocaky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morron,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 157839)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Chospel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferrelra,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehocaky,J., Levine,R., Liu,G., Maclean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Traversman,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

```

```

TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 9, 2002 this sequence version replaced gi:14029953.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1404
Center clone name: 119_A_16
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 7973: contig of 7973 bp in length
* 7974 8073: gap of 100 bp
* 8074 81857: contig of 73784 bp in length
* 81858 81957: gap of 100 bp
* 81958 136278: contig of 54321 bp in length
* 136279 136378: gap of 100 bp
* 136379 157839: contig of 21461 bp in length.
* Location/Qualifiers
  1. 157839
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /clones="RP11-119A16"
    /clone_lib="RPC1-11 Human Male BAC"

ORIGIN
Query Match          47.7%; Score 124.4; DB 2; Length 157839;
Best Local Similarity 95.5%; Pred. No. 8.7e-29;
Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 128 AAATATTTCCAGCTTTTTCATGTTTCGCAACAGGTGCTCCGCTCGTTGTGTCAGCGATGG 187
    |||||
Db 41082 AAATATTTCCAGCTTTTTCATGTTTCGCAACAGGTGCTCCGCTCGTTGTGTCAGCGATGG 41141

QY 188 AGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTCTTTTACC 247
    |||||
Db 41142 AGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTCTTTTACC 41201

QY 248 TCAAGTGTGTGTA 261
    |||||
Db 41202 TCAAGTGTGTGTA 41215

RESULT 12
AC083841/c
LOCUS
DEFINITION Homo sapiens chromosome 8, clone RP11-706C16, complete sequence.
ACCESSION AC083841
VERSION AC083841.9 GI:21206312
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 203375)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-706C16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 203375)

```



```
/rpt family=" (TG)n"
complement(14739..15100)
/rpt family="MLT1A1"
complement(15107..16745)
/rpt family="MLT1A1-int"
complement(16775..17008)
/rpt family="MLT1A1"
17407..19132
/rpt family="ERVL"
19133..19543
/rpt family="MSTC"
19544..19657
/rpt family="ERVL"
19663..19727
/rpt family="MLT2C1"
complement(19728..20141)
/rpt family="MSTA"
20142..20401
/rpt family="MLT2C1"
20402..20436
/rpt family=" (CA)n"
20437..20514
/rpt family="MLT2C1"
20520..20882
/rpt family="THE1C"
20925..21058
/rpt family="L1"
21060..21440
/rpt family="L1M2"
21940..22004
/rpt family="L1PB3"
22032..22331
/rpt family="L1PB3"
22570..25009
/rpt family="L1PB3"
25105..25625
/rpt family="L1PB3"
complement(25625..25798)
/rpt family="L1"
25826..27177
```

Query Match 47.7%; Score 124.4; DB 9; Length 203375;

Best Local Similarity 95.5%; Pred. No. 8.7e-29;

Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
QY 128 AAATATTTCCAGTTTTTCATGTTTCGCAACAGAGTCTCCCTCGTGTGTGCAGCGATGG 187
D 184739 AAATATTTCCAGTTTTTCATGTTTCGCAACAGAGTCTCCCTCGTGTGTGCAGCGATGG 184680
QY 188 AGAGACCCCAAGCCAGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTTTTACC 247
D 184679 AGAGACCCCAAGCCAGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTTTTACC 184620
QY 248 TCAAGTGTGTGTA 261
D 184619 TCAAGTGTGTGTA 184606
```

RESULT 13

AF176678

LOCUS Homo sapiens chromosome 8 clone CTA-93D7 map 8q24.3, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.

ACCESSION AF176678

VERSION AF176678.3 GI:14277241

KEYWORDS HTG; HTGS; PHASE1; HTGS_DRAFT; HTGS_CANCELLED.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Schilhabel,M.B., Baumgart,C., Dette,M., Jahn,N.,
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,

Siddiqui,R., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R.,
Rosenthal,A. and Platzner,M.
Chromosome 8 genomic sequence
Unpublished
2 (bases 1 to 103247)
Polley,A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M.,
Menzel,U. and Rosenthal,A.
Direct Submission
Submitted (09-AUG-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
On Jun 1, 2001 this sequence version replaced gi:8151715.

----- Genome Center

Center: Insitute of Molecular Biotechnology

Center code: IMB

Web site: http://genome.imb-jena.de/

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: H187

Center clone name: CTA-93D7

----- Summary Statistics

Sequencing vector: M13; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 99831 bases at least Q40

Consensus quality: 94832 bases at least Q30

Consensus quality: 98334 bases at least Q20

Coverage: 5.01 in Q20 bases; sum-of-contigs

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1510: contig of 1510 bp in length

* 1511 1610: gap of unknown length

* 1611 4022: contig of 2412 bp in length

* 4023 4122: gap of unknown length

* 4123 8486: contig of 4364 bp in length

* 8487 8586: gap of unknown length

* 8587 12803: contig of 4217 bp in length

* 12804 12903: gap of unknown length

* 12904 16146: contig of 3243 bp in length

* 16147 16246: gap of unknown length

* 16247 23920: contig of 7674 bp in length

* 23921 29710: contig of 5690 bp in length

* 29711 29810: gap of unknown length

* 29811 33268: contig of 3458 bp in length

* 33269 33368: gap of unknown length

* 33369 42999: contig of 9531 bp in length

* 42900 42999: gap of unknown length

* 43000 54681: contig of 11682 bp in length

* 54682 54781: gap of unknown length

* 54782 60929: contig of 6148 bp in length

* 60930 61029: gap of unknown length

* 61030 79991: contig of 18962 bp in length

* 79992 80091: gap of unknown length

* 80092 103247: contig of 23156 bp in length.

* Location/Qualifiers

* 1..103247

FEATURES

source

```
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q24.3"
/clone="CTA-93D7"

Query Match      46.4%; Score 121.2; DB 2; Length 103247;
Best Local Similarity 94.0%; Pred. No. 9.3e-28;
Matches 126; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

ORIGIN
QY 128 AAATATTTCCAGCTTTTTCATGGTTTCGCAACAGGTGCTCCGCTGGTGTGTGTCAGCGCATGG 187
DB 19241 AAATATTTCCAGCTTTTTCATGGTTTCGCAACAGGTGCTCCGCTGGTGTGTGTCAGCGCATGG 19300
QY 188 AGAGACCCAGCAGGAGGAGCGGTCTCTCTGGAAGCCATGCGCTTCTTTTACC 247
DB 19301 AGAGACCCAGCAGGAGGAGTGGGTCTCTCTTGAAGAGCCATGCGCTTCTTTTACC 19360
QY 248 TCAAGTGTGTGTA 261
DB 19361 TCAAGTGTGTGTA 19374

RESULT 14
BV203566
LOCUS
DEFINITION
sqmzm12498 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION
BV203566
VERSION
BV203566.1 GI:48172981
KEYWORDS
STS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 201)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press
CONTACT: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.

FEATURES
source
1..201
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1..>201

STS
ORIGIN
Query Match      40.2%; Score 105; DB 11; Length 201;
Best Local Similarity 98.1%; Pred. No. 1.4e-22;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCAGCGACCGACGAGGGTGACATAGAGTGGTGTCTATGCTGTGAGAGAGAAAACAC 62
DB 95 CCAGCGACCGACGAGGGTGACATAGAGTGGTGTCTATGCTGTGAGAGAGAAAACAC 154
QY 63 TTTCGAGTGCACAGACCCCAAGGAGGTGCAATGAGCCATGACTACT 109
|||||
```

```
155 TTTCGAGTGCACAGACCCCAAGGAGGTGCAATGAGCCATGACTACT 201
Mus musculus RIKEN cDNA 2410015A16 gene, mRNA (cDNA clone MGC:58713
IMAGE:6743692), complete cds.

BC049723      643 bp      mRNA      linear      ROD 07-OCT-2003
Mus musculus RIKEN cDNA 2410015A16 gene, mRNA (cDNA clone MGC:58713
IMAGE:6743692), complete cds.

ACCESSION
BC049723
VERSION
BC049723.1
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 643)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 643)
Strausberg,R.
Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Ustin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalusz, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Nataasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 46 Row: d Column: 24.
Location/Qualifiers
1..643
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"

FEATURES
source
```

```
/clone="MGC:58713 IMAGE:6743692"
/tissue_type="Testis, mouse"
/clone_lib="NIH_MGC_169"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
1. .643
/gene="2410015A16Rik"
/db_xref="LocusID:76486"
/db_xref="MGI:1923736"
58. .522
/gene="2410015A16Rik"
/codon_start=1
/product="2410015A16Rik protein"
/protein_id="AAH49723.1"
/db_xref="GI:29437323"
/db_xref="LocusID:76486"
/db_xref="MGI:1923736"
/translation="MAFLVALLVLGLQVSNALTCHVCEAONSACSNPSQCPGEK
KFCLLAVTRIFERPFYVSKQCTRPVSPSTNPSPSEPKERLIEKMPFLFYKCC
QWDSNCGEPTDQLLKEQPGKASGRHRYIELLTGFWLTTANGLSALCLL"
```

ORIGIN

Query Match		14.3%	Score 37.2;	DB 10;	Length 643;
Best Local Similarity		53.4%	Pred. No. 1.2;		
Matches	78;	Conservative	0;	Mismatches	68; Indels 0; Gaps 0;
Qy	37	TGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCCAGACCCAAAGGAGGTGCAATGG	96		
Db	124	TGCCATGTGTGTGAGCGCGAGAACAGCTATGCTCGAATCCGTCAGTCCCGCTGGA	183		
Qy	97	ACAGAGCCATCTGCGTTATAGCGCGGTGAAATATTTCCACGTTTTTTCATGTTGCG	156		
Db	184	GAAGAAGAAATCTGTTGTGGCCGTCACACGAATTTTGAACGTTCTCTATGTGTCG	243		
Qy	157	AACAGGTGCTCCGCTGTTGTGCAGC	182		
Db	244	AAACAGTGACCCGAGGTTGCCAC	269		

Search completed: August 27, 2005, 09:49:26
Job time : 1389.39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:08:44 ; Search time 2434.6 Seconds
(without alignments)
4080.665 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 261

Sequence: 1 agccgcgaacgacgagg.....tttacctcaagtgtgttaa 261

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247.8	94.9	559	2	BE550793
2	247.8	94.9	560	1	AI583197
3	247.8	94.9	560	1	AI703260
4	247.8	94.9	575	2	BE551234
5	247.8	94.9	619	1	AI828018
6	247.8	94.9	640	4	BG492128
7	247.8	94.9	647	4	BG027935
8	247.8	94.9	679	5	BM915575
9	247.8	94.9	682	5	BQ676087
10	247.8	94.9	682	5	BQ679186
11	247.8	94.9	684	5	BU500474
12	247.8	94.9	909	5	BQ276968
13	247.8	94.9	2326	3	CR590427
14	246.2	94.3	626	2	BE547043
15	245.2	93.9	636	4	BI560005
16	240.2	92.0	1042	5	BE546303
17	236.8	90.7	664	2	BE546303
18	235.2	90.1	807	4	BG491699
19	235.2	90.1	1232	4	BM909166
20	228.8	87.7	486	1	AA723810
21	221.2	84.8	474	1	AI990402
22	218.8	83.8	739	4	BG491223
23	217.8	83.4	468	1	AI652550
24	214.2	82.1	541	2	BE670793

25	210.2	80.5	1100	4	BM555598
C 26	206.8	79.2	591	4	BG492263
C 27	200	76.6	542	2	BE670388
C 28	199.4	76.6	447	2	BE670388
C 29	188.4	72.2	295	2	AW518819
C 30	181.4	69.5	441	4	BG110594
C 31	179.2	68.7	675	2	BF718611
C 32	177.4	68.0	999	5	BM911850
C 33	174.2	66.7	1070	4	BM554262
C 34	171.2	65.6	482	1	AI740834
C 35	165.8	63.5	422	1	AI081839
C 36	164.4	63.0	517	7	W44613
C 37	152	58.2	187	2	BE937764
C 38	146.2	56.0	439	2	AW450430
C 39	146.2	56.0	1112	4	BM808520
C 40	127.8	49.0	394	2	AW445220
C 41	126.8	48.6	463	1	AI860440
C 42	126.8	48.6	857	5	BU543716
C 43	126.8	48.6	984	5	BQ942376
C 44	126.6	48.5	377	1	AA723706
C 45	125.4	48.0	378	1	AI674656

ALIGNMENTS

RESULT 1
BE550793
LOCUS
DEFINITION
7b59a07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3232500 3', similar to TR:O15227 O15227 cDNA FOR DIFFERENTIALLY EXPRESSED COL6 GENE.; mRNA sequence.

ACCESSION
BE550793

VERSION
BE550793.1

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 559)

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 487.
Location/Qualifiers
1..559
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3232500"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI CGAP Lu5 was prepared and ss circles were used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento

FEATURES
source

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 94.9%; Score 247.8; DB 1; Length 560;
Best Local Similarity 97.3%; Pred. No. 1.9e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 62
DB 263 CCAGCGAACGGACGGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 322
QY 63 TTTCGAGTGCCAGAACCCCAAGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 122
DB 323 TTTCGAGTGCCAGAACCCCAAGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 382
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 182
DB 383 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 442
QY 183 GATGAGAGACCCCAAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 443 GATGAGAGACCCCAAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 502
QY 243 TTACCTCAAGTGTGTAAA 261
DB 503 TTACCTCAAGTGTGTAAA 521

RESULT 4

BE551234 575 bp mRNA linear EST 10-AUG-2000
LOCUS 7b56d09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3232241 3'
DEFINITION similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16 GENE.; mRNA sequence.
ACCESSION BE551234
VERSION BE551234.1 GI:9729226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 575)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: -40UP from Gibco
High quality sequence stop: 507.

FEATURES

Location/Qualifiers
1..575
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3232241"
/tissue_type="carcinoid"

/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 94.9%; Score 247.8; DB 2; Length 575;
Best Local Similarity 97.3%; Pred. No. 1.9e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 62
DB 284 CCAGCGAACGGACGGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 343
QY 63 TTTCGAGTGCCAGAACCCCAAGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 122
DB 344 TTTCGAGTGCCAGAACCCCAAGAGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAACAC 403
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 182
DB 404 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 463
QY 183 GATGAGAGACCCCAAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 464 GATGAGAGACCCCAAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 523
QY 243 TTACCTCAAGTGTGTAAA 261
DB 524 TTACCTCAAGTGTGTAAA 542

RESULT 5

AI828018 619 bp mRNA linear EST 18-DEC-1999
LOCUS wf12f09.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2350409 3' similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16 GENE.; mRNA sequence.
ACCESSION AI828018
VERSION AI828018.1 GI:5448610
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 619)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 467.

Location/Qualifiers
1..619
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2350409"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

FEATURES

source
1..619
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2350409"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-GCAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 94.9%; Score 247.8; DB 1; Length 619;
Best Local Similarity 97.3%; Pred. No. 1.9e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAAACAC 62
|||
DB 263 CCAGCGAACGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAAACAC 322
|||

QY 63 TTTGAGTGCCAGACCCAGAGAGGTGCAATAGGACAGAGCCATAGCTGGTTATAGCGGC 122
|||

DB 323 TTTGAGTGCCAGACCCAGAGAGGTGCAATAGGACAGAGCCATAGCTGGTTATAGCGGC 382
|||

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGCGACG 182
|||

DB 383 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGCGACG 442
|||

QY 183 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
|||

DB 443 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 502
|||

QY 243 TTACCTCAAGTGTGTGAAA 261
|||

DB 503 TTACCTCAAGTGTGTGAAA 521
|||

RESULT 6

BG492128/c
LOCUS BG492128 640 bp mRNA linear EST 27-MAR-2001
DEFINITION 602535267T1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4654072 3',
mRNA sequence.

ACCESSION BG492128
VERSION BG492128.1 GI:13453640
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 640)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1441 row: e column: 17
High quality sequence start: 29
High quality sequence stop: 640.
Location/Qualifiers
1. .640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4654072"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant) "

FEATURES
source

1. .640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4654072"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant) "

/clone lib="NIH_MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.9%; Score 247.8; DB 4; Length 640;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAAACAC 62
|||

DB 452 CCAGCGAACGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAAACAC 393
|||

QY 63 TTTGAGTGCCAGACCCAGAGAGGTGCAATAGGACAGAGCCATAGCTGGTTATAGCGGC 122
|||

DB 392 TTTGAGTGCCAGACCCAGAGAGGTGCAATAGGACAGAGCCATAGCTGGTTATAGCGGC 333
|||

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGCGACG 182
|||

DB 332 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGCGACG 273
|||

QY 193 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
|||

DB 272 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 213
|||

QY 243 TTACCTCAAGTGTGTGAAA 261
|||

DB 212 TTACCTCAAGTGTGTGAAA 194
|||

RESULT 7

BG027935
LOCUS BG027935 647 bp mRNA linear EST 24-JAN-2001
DEFINITION 602294533F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389033 5',
mRNA sequence.

ACCESSION BG027935
VERSION BG027935.1 GI:12417029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 647)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10076 row: b column: 10
High quality sequence stop: 608.
Location/Qualifiers
1. .647
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4389033"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant) "
/clone_lib="NIH_MGC_86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;

FEATURES
source

1. .647
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4389033"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant) "
/clone_lib="NIH_MGC_86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;

Site.2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.53 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."

ORIGIN	Query Match	94.9%;	Score 247.8;	DB 4;	Length 647;
	Best Local Similarity	97.3%;	Pred. No. 2e-68;		
	Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	3	CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAAAC	62		
Db	138	CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAAAC	197		
Qy	63	TTTTCGATGTCAGAACCCNAGGAGGTGCCAATGGACACAGAGCCATACCTCGTTATAGCGGC	122		
Db	198	TTTTCGATGTCAGAACCCNAGGAGGTGCCAATGGACACAGAGCCATACCTCGTTATAGCGGC	257		
Qy	123	CGTGAATAATTTCCAGCTTTTTTCATGTTTCGCAACACAGGTGTCCTCGTGTGTGCAGC	182		
Db	258	CGTGAATAATTTCCAGCTTTTTTCATGTTTCGCAACAGCTGCTCCCGTGTGTGCAGC	317		
Qy	183	GATGGAGAGACCCAAGCCAGAGGAGAAAGCGGTTTTCTCTCGTGAAGAGCCCATGCCCTTCTT	242		
Db	318	GATGGAGAGACCCAAGCCAGAGGAGAAAGCGGTTTTCTCTCGTGAAGAGCCCATGCCCTTCTT	377		
Qy	243	TTACCTCAAGTGTGTGTAAG	261		
Db	378	TTACCTCAAGTGTGTGTAAG	396		

RESULT 8	
BM915575	
LOCUS	
DEFINITION	679 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6701603 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481773 S', mRNA sequence.
ACCESSION	BM915575
VERSION	BM915575.1 GI:19365954
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 679)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-f@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2006 row: m column: 06 High quality sequence stop: 680. Location/Qualifiers 1..679
FEATURES	
SOURCE	

```

FEATURES
source
align quality sequence start: 880.
Location/Qualifiers
1. .679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="IWAGE:5481773"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
(clone_lib="NIH MGC 41"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

```

Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

nif_hsc library.					
ORIGIN	Query Match	94.9%	Score 247.8;	DB 5;	Length 679;
	Best Local Similarity	97.3%;	Pred. No. 2e-68;		
	Matches 252;	Conservative 0;	Mismatches 0;	Gaps 0;	
Qy	3	CCAGCGAACGGACGAGGGTGACAATGAGTGTGGTGTCACTTTGTGAGAGAGAAACAC	62		
Db	165	CCAGCGAACCAGCGAGGGTGACAATGAGTGTGGTGTCACTTTGTGAGAGAGAAACAC	224		
Qy	63	TTTTCGAGTGCAGAACCCCRAGGAGGTGCCAATGGACAGAGCCCATACTGCGTTATAGCGGC	122		
Db	225	TTTTCGAGTGCAGAACCCCAAGAGAGGTGCCAATGGACAGAGCCCATACTGCGTTATAGCGGC	284		
Qy	123	CGTGAATAATTTCACGTTTTTTTCATGGTTTCACAACAGGTGCTCGCTGGTTGTGCAGC	182		
Db	285	CGTGAATAATTTCACGTTTTTTTCATGGTTGGAAGCAGTGTCTCGCTGGTTGTGCAGC	344		
Qy	183	GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCTGGAAAGAGCCCATGCCCTTCTT	242		
Db	345	GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCTGGAAAGAGCCCATGCCCTTCTT	404		
Qy	243	TTACCTCAAGTGTGTGAAA	261		
Db	405	TTACCTCAAGTGTGTGAAA	423		

RESULT 9	
BQ676087	
LOCUS	
DEFINITION	BQ676087 682 bp mRNA linear EST 15-JUL-2002 AGENCOURT 8507940 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294463 5', mRNA sequence.
ACCESSION	BQ676087
VERSION	BQ676087.1 GI:21788766
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 682)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CM2499 row: c column: 08 High quality sequence stop: 637. Location/Qualifiers 1..682
FEATURES	
SOURCE	

```

FEATURES
source
magn query sequence stop: 637.
Location/Qualifiers
1. .682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6294463"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GACACAGAG) Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

```

```
ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 682;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGTTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAACAC 62
   |||||
Db 157 CCAGCGAACGGACGAGGTTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAACAC 216
   |||||
QY 63 TTTCGAGTGCACAGAACCCCAAGGAGGTGCAAAATGACAGAGCCATACCTGCGTTATAGCGGC 122
   |||||
Db 217 TTTCGAGTGCACAGAACCCCAAGGAGGTGCAAAATGACAGAGCCATACCTGCGTTATAGCGGC 276
   |||||
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTTGTGCAGC 182
   |||||
Db 277 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTTGTGCAGC 336
   |||||
QY 183 GATGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
   |||||
Db 337 GATGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 396
   |||||
QY 243 TTAACCTCAAGTGTGTGAAA 261
   |||||
Db 397 TTAACCTCAAGTGTGTGAAA 415
   |||||

RESULT 10
BQ679186
LOCUS
DEFINITION BQ679186 682 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence.
ACCESSION BQ679186
VERSION BQ679186
KEYWORDS BQ679186.1 GI:21791865
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2333 row: j column: 06
High quality sequence stop: 660.
Location/Qualifiers
1. 682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6091109"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 684;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGTTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAACAC 62
   |||||
Db 157 CCAGCGAACGGACGAGGTTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAACAC 216
   |||||
QY 63 TTTCGAGTGCACAGAACCCCAAGGAGGTGCAAAATGACAGAGCCATACCTGCGTTATAGCGGC 122
   |||||
Db 217 TTTCGAGTGCACAGAACCCCAAGGAGGTGCAAAATGACAGAGCCATACCTGCGTTATAGCGGC 276
   |||||
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTTGTGCAGC 182
   |||||
Db 277 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTTGTGCAGC 336
   |||||
QY 183 GATGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
   |||||
Db 337 GATGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 396
   |||||
QY 243 TTAACCTCAAGTGTGTGAAA 261
   |||||
Db 397 TTAACCTCAAGTGTGTGAAA 415
   |||||

RESULT 11
BQ500474
LOCUS
DEFINITION BQ500474 684 bp mRNA linear EST 12-SEP-2002
5', mRNA sequence.
ACCESSION BQ500474
VERSION BQ500474.1 GI:22801450
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: NIMH/LOG
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2355 row: e column: 11
High quality sequence start: 2
High quality sequence stop: 648.
Location/Qualifiers
1. 684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6109426"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_64"
/notes="Vector: pOTB7a; Site 1: CeuI; Site 2: ScaI; This
library is a size selection of NIH_MGC_35, from 3.0-4.5
kb. Size selection done at the National Institute of
Mental Health, NIH. Note: this is a NIH_MGC Library."

ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 684;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGTTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAACAC 62
   |||||
```

```

Db      144 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 203
QY      63 TTTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 122
Db      204 TTTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 263
QY      123 CGTGAAAATATTTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
Db      264 CGTGAAAATATTTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 323
QY      183 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db      324 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 383
QY      243 TTACCTCAAGTGTGTGAAA 261
Db      384 TTACCTCAAGTGTGTGAAA 402

RESULT 12
LOCUS   BQ276968
DEFINITION AGENCOURT_6770142 NIH_MGC_126 Homo sapiens cDNA clone IMAGE:5810055
5', mRNA sequence.
ACCESSION BQ276968
VERSION   BQ276968.1 GI:20487176
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE      NIH-MGC http://mgi.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2056 row: k column: 16
High quality sequence stop: 505.
Location/Qualifiers
1. .909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5810055"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="PH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattagcc);
Site 2: SfiI (ggcgctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCTAGGTATCAGCAGAGTGCATTAGCGCGG-3' and
5'-ATTCTAGAGCGGAGCGGCGGACATG-3'." Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

FEATURES source
1. .909
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5810055"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="PH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattagcc);
Site 2: SfiI (ggcgctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCTAGGTATCAGCAGAGTGCATTAGCGCGG-3' and
5'-ATTCTAGAGCGGAGCGGCGGACATG-3'." Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 94.9%; Score 247.8; DB 3; Length 2326;
Best Local Similarity 97.3%; Pred. No. 2.8e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 62
Db 165 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 224

```

```

Query Match 94.9%; Score 247.8; DB 5; Length 909;
Best Local Similarity 97.3%; Pred. No. 2.2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 62
Db 123 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 182
QY 63 TTTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 122
Db 183 TTTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 242
QY 123 CGTGAAAATATTTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
Db 243 CGTGAAAATATTTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 302
QY 183 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 303 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 362
QY 243 TTACCTCAAGTGTGTGAAA 261
Db 363 TTACCTCAAGTGTGTGAAA 381

RESULT 13
LOCUS   CR590427
DEFINITION full-length cDNA clone CSODK010YP02 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR590427
VERSION   CR590427.1 GI:50471234
KEYWORDS  HTC; CNSLT_cDNA.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE      Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL    Full-length cDNA libraries and normalization
REMARK     Unpublished
Contact: Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 2326)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT    1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .2326
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK010YP02"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 94.9%; Score 247.8; DB 3; Length 2326;
Best Local Similarity 97.3%; Pred. No. 2.8e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 62
Db 165 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTGTTGTGAGAGAGAAAACAC 224

```

```

QY 63 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 122
DB 225 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 284
QY 123 CGTGAATAATTTCCACAGTTTTTTCATGTTCCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
DB 285 CGTGAATAATTTCCACAGTTTTTTCATGTTCCGCAACAGGTGCTCCGCTGGTTGTGCAGC 344
QY 183 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCGCTTTCTT 242
DB 345 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCGCTTTCTT 404
QY 243 TTACCTCAAGTGTGTAA 261
DB 405 TTACCTCAAGTGTGTAA 423

RESULT 14
LOCUS BE547043 626 bp mRNA linear EST 09-AUG-2000
DEFINITION 601076162F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3462278 5',
mRNA sequence.
ACCESSION BE547043
VERSION BE547043.1 GI:9775779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8459 row: k column: 15
High quality sequence stop: 585.
Location/Qualifiers
1. 626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3462278"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: Cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 94.3%; Score 246.2; DB 2; Length 626;
Best Local Similarity 96.9%; Pred. No. 6.4e-68;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 62
DB 130 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 189
QY 63 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 122
DB 190 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 249
QY 123 CGTGAATAATTTCCACAGTTTTTTCATGTTCCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182

```

```

DB 250 CGTGAATAATTTCCACAGTTTTTTCATGTTCCGCAACAGGTGCTCCGCTGGTTGTGCAGC 309
QY 183 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCGCTTTCTT 242
DB 310 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCGCTTTCTT 369
QY 243 TTACCTCAAGTGTGTAA 261
DB 370 TTACCTCAAGTGTGTAA 388

RESULT 15
LOCUS BI560005 636 bp mRNA linear EST 05-SEP-2001
DEFINITION 603253476F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295811 5',
mRNA sequence.
ACCESSION BI560005
VERSION BI560005.1 GI:15447319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11748 row: h column: 20
High quality sequence stop: 636.
Location/Qualifiers
1. 636
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5295811"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match 93.9%; Score 245.2; DB 4; Length 636;
Best Local Similarity 96.9%; Pred. No. 1.3e-67;
Matches 250; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 62
DB 114 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 173
QY 63 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 122
DB 174 TTTCAGTCCAGAACCCAGAGAGTGCMAATGGACAGAGCCATCTCGTTATAGCGC 233
QY 123 CGTGAATAATTTCCACAGTTTTTTCATGTTCCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182

```

Db	234	CGTGAAATATTTCCACGTTTTTTCATGTTCCGAGACAGTCTCCGCTGGTGTGTCAGC	293
Qy	183	GATGGAGAGACCCAGCCAGAGGAGACGGTTTCTCTGGAGAGACCCATGCCCTTCTT	242
Db	294	GATGGAGAGACCCAGCCAGAGGAGACGGTTTCTCTCTGGAAGAGCCATGCCCTTCTT	353
Qy	243	TTACTCAAGTGTGTGTA	260
Db	354	TTACTCAAGTGTGTGTA	371

Search completed: August 27, 2005, 11:16:23
Job time : 2437.6 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:38:03 ; Search time 478.968 Seconds
(without alignments)
3565.473 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 261
Sequence: 1 agccagcgaacgacgaggg.....tttacctcaagtgtgtaaa 261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261	100.0	261	13	US-10-079-954-2
2	247.8	94.9	672	17	Sequence 2, Appli
3	247.8	94.9	672	18	Sequence 339, App
4	247.8	94.9	754	17	Sequence 172, App
5	247.8	94.9	754	17	Sequence 2414, Ap
6	247.8	94.9	1026	9	Sequence 2414, Ap
7	247.8	94.9	1026	14	Sequence 1, Appli

RESULT 1

US-10-079-954-2
; Sequence 2, Application US/10079954
; Publication No. US2002016861A1
; GENERAL INFORMATION:
; APPLICANT: Nees, Matthias
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/10/079,954
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US/09/308,984
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-954-2

ALIGNMENTS

8	247.8	94.9	1373	17	US-10-295-027-753	Sequence 753, App
9	246.2	94.3	502	17	US-10-264-049-1723	Sequence 1723, Ap
10	233.6	89.5	1745	20	US-10-723-860-7232	Sequence 7232, Ap
11	34.8	13.3	417	14	US-10-238-443-13	Sequence 13, Appl
12	34.8	13.3	417	15	US-10-309-362-13	Sequence 13, Appl
13	34.8	13.3	627	14	US-10-238-443-11	Sequence 11, Appl
14	34.8	13.3	627	15	US-10-309-362-11	Sequence 11, Appl
15	34.8	13.3	1710	14	US-10-238-443-10	Sequence 10, Appl
16	34.8	13.3	1710	15	US-10-309-362-10	Sequence 10, Appl
17	34.8	13.3	3676	14	US-10-238-443-3	Sequence 3, Appli
18	34.8	13.3	3676	15	US-10-309-362-3	Sequence 3, Appli
19	34.8	13.3	3715	17	US-10-443-108-1	Sequence 4, Appli
20	33.8	13.0	1260	17	US-10-188-646-4	Sequence 1, Appli
21	33.8	13.0	1268	19	US-10-807-897-28	Sequence 28, Appl
22	33.8	13.0	1322	19	US-10-807-897-26	Sequence 26, Appl
23	33.8	13.0	1337	14	US-10-235-026-1	Sequence 1, Appli
24	33.8	13.0	1363	20	US-10-839-882-37	Sequence 37, Appl
25	33.8	13.0	1376	14	US-10-244-586-1	Sequence 1, Appli
26	33.8	13.0	4810	17	US-10-188-646-11	Sequence 11, Appl
27	32.6	12.5	458	14	US-10-184-644-496	Sequence 496, App
28	32.6	12.5	458	14	US-10-184-634-496	Sequence 496, App
29	32	12.3	170	22	US-10-651-991-90	Sequence 90, Appl
30	31.2	12.0	651	19	US-10-767-701-2245	Sequence 2245, Ap
31	31.2	12.0	114793	15	US-10-148-806-3	Sequence 3, Appli
32	31.2	12.0	114793	22	US-10-859-792-3	Sequence 3, Appli
33	31	11.9	637	13	US-10-027-632-255637	Sequence 255637,
34	31	11.9	637	17	US-10-027-632-255637	Sequence 19, Appl
35	31	11.9	2142	9	US-09-989-722-19	Sequence 19, Appl
36	31	11.9	2142	9	US-09-989-723-19	Sequence 19, Appl
37	31	11.9	2142	9	US-09-989-727-19	Sequence 19, Appl
38	31	11.9	2142	9	US-09-989-727-19	Sequence 19, Appl
39	31	11.9	2142	9	US-09-989-731-19	Sequence 19, Appl
40	31	11.9	2142	9	US-09-989-732-19	Sequence 19, Appl
41	31	11.9	2142	9	US-09-991-073-19	Sequence 19, Appl
42	31	11.9	2142	9	US-09-990-442-19	Sequence 19, Appl
43	31	11.9	2142	9	US-09-991-163-19	Sequence 19, Appl
44	31	11.9	2142	9	US-09-993-604-19	Sequence 19, Appl
45	31	11.9	2142	9	US-09-990-456-19	Sequence 19, Appl

Query Match 100.0%; Score 261; DB 13; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e-82;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGCCAGCGAACGACGAGGGTGCAATAGAGTGTGTCATGCTTGTGAGAGAGAAAC 60
|||||

Db 1 AGCCAGCGAACGAGCGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAAC 60
Qy 61 ACTTTGAGTGCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGG 120
Db 61 ACTTTGAGTGCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGG 120
Qy 121 GCCGTGAAATATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 180
Db 121 GCCGTGAAATATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 180
Qy 181 GCGATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
Db 181 GCGATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
Qy 241 TTTTACCTCAAGTGTGTAA 261
Db 241 TTTTACCTCAAGTGTGTAA 261

RESULT 2

US-10-295-027-339
; Sequence 339, Application US/10295027
; Publication No. US2003032350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-339

Query Match 94.9%; Score 247.8; DB 17; Length 672;
Best Local Similarity 97.3%; Pred. No. 8.5e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 CCAGCGAACGAGCGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62

Db 267 CCAGCGAACGAGCGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 326
Qy 63 TTTTCGAGTGCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 122
Db 327 TTTTCGAGTGCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 386
Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 446
Qy 183 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
Qy 243 TTACTCAAGTGTGTAA 261
Db 507 TTACTCAAGTGTGTAA 525

RESULT 3

US-10-188-832-172
; Sequence 172, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 172
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-832-172

Query Match 94.9%; Score 247.8; DB 18; Length 672;
Best Local Similarity 97.3%; Pred. No. 8.5e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 CCAGCGAACGAGCGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62
Db 267 CCAGCGAACGAGCGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 326
Qy 63 TTTTCGAGTGCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 122
Db 327 TTTTCGAGTGCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 386
Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTCCCAACAGGTGCTCCGCTGGTTGTGCA 446
Qy 183 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
Qy 243 TTACTCAAGTGTGTAA 261

Db 507 TTACCTCAAGTGTGTAAA 525
|||||

RESULT 4
US-10-172-118-2414/c
; Sequence 2414, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2414
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Contig49058
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2414

Query Match 94.9%; Score 247.8; DB 17; Length 754;
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 62
Db 498 CCAGCGAACGGACGAGGGTGACANTAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 439

QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 122
Db 438 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 379

QY 123 CGTGAATAATATTCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTGTGCGAC 182
Db 378 CGTGAATAATATTCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTGTGCGAC 319

QY 183 GATGAGAGACCCCAAGCCAGAGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 318 GATGAGAGACCCCAAGCCAGAGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 259

QY 243 TTACCTCAAGTGTGTAAA 261
Db 258 TTACCTCAAGTGTGTAAA 240

RESULT 5
US-10-342-887-2414/c
; Sequence 2414, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999

; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2414
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-2414

Query Match 94.9%; Score 247.8; DB 18; Length 754;
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 62
Db 498 CCAGCGAACGGACGAGGGTGACANTAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 439

QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 122
Db 438 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 379

QY 123 CGTGAATAATATTCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTGTGCGAC 182
Db 378 CGTGAATAATATTCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTGTGCGAC 319

QY 183 GATGAGAGACCCCAAGCCAGAGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 318 GATGAGAGACCCCAAGCCAGAGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 259

QY 243 TTACCTCAAGTGTGTAAA 261
Db 258 TTACCTCAAGTGTGTAAA 240

RESULT 6
US-09-977-801-1
; Sequence 1, Application US/09977801
; Publication No. US20020086848A1
; GENERAL INFORMATION:
; APPLICANT: Fanconi-gene II
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,632
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..924
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 430..924
US-09-977-801-1

Query Match 94.9%; Score 247.8; DB 9; Length 1026;
Best Local Similarity 97.3%; Pred. No. 1e-77;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 62
DB 522 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 581

QY 63 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 122
DB 592 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 641

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 182
DB 642 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 701

QY 183 GATGAGAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 122
DB 592 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 641

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 182
DB 642 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 701

QY 183 GATGAGAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 122
DB 592 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 641

QY 243 TTACTCAAGTGTGTAA 261
DB 762 TTACTCAAGTGTGTAA 780

RESULT 7
US-10-199-448-1
; Sequence 1, Application US/10199448
; Publication No. US20030022858A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Mannheim GmbH
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; STREET: Sandhofer Str. 112-132
; CITY: Mannheim
; COUNTRY: Germany
; ZIP: 68305
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,448
; FILING DATE: 19-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/402,632
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..924
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 430..924
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-199-448-1

Query Match 94.9%; Score 247.8; DB 14; Length 1026;
Best Local Similarity 97.3%; Pred. No. 1e-77;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 62
DB 522 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 581

QY 63 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 122
DB 592 TTTCGAGTCCAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 641

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 182
DB 642 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGGTCTCCGCTGGTGTGCGAGC 701

QY 183 GATGAGAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 122
DB 702 GATGAGAGACCCAGAGAGTGCNAATGGACAGACCATACTCGGTTATAGCGGC 641

QY 243 TTACTCAAGTGTGTAA 261
DB 762 TTACTCAAGTGTGTAA 780

RESULT 8
US-10-295-027-753
; Sequence 753, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 753
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-753

Query Match 94.9%; Score 247.8; DB 17; Length 1373;
Best Local Similarity 97.3%; Pred. No. 1.1e-77;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 62
DB 136 CCAGCGAACGGACGAGGGTGCAATAGAGTGTGGTTCATGCTGTGAGAGAGAAACAC 195

```

QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 122
Db 196 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 255
QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAGC 182
Db 256 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAGC 315
QY 183 GATGGAGAGACCAACGAGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 242
Db 316 GATGGAGAGACCAACGAGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 375
QY 243 TTACCTCAAGTGTGTAAA 261
Db 376 TTACCTCAAGTGTGTAAA 394

```

RESULT 9

```

US-10-264-049-1723
; Sequence 1723, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/19569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1723
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-1723

```

```

Query Match 94.3%; Score 246.2; DB 17; Length 502;
Best Local Similarity 96.9%; Pred. No. 2.8e-77;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAAAACAC 62
Db 85 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAAAACAC 144
QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 122
Db 145 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 204
QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAGC 182
Db 205 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAGC 264
QY 183 GATGGAGAGACCAACGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 242
Db 265 GATGGAGAGACCAACGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 324
QY 243 TTACCTCAAGTGTGTAAA 261
Db 325 TTACCTCAAGTGTGTAAA 343

```

RESULT 10

```

US-10-723-860-7232
; Sequence 7232, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert

```

```

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7232
; LENGTH: 1745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7232

```

```

Query Match 89.5%; Score 233.6; DB 20; Length 1745;
Best Local Similarity 96.2%; Pred. No. 1.5e-72;
Matches 250; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 3 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAAAACAC 62
Db 507 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAAAACAC 566
QY 63 -TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGG 121
Db 567 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGG 626
QY 122 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAG 181
Db 627 CGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGGTCTCGCTGGTTGTGCAG 686
QY 182 CGATGGAGAGACCAACGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 241
Db 687 CGATGGAGAGACCAACGAGAGAGCGGTTTCTCCTGGAAGAGCCATGCCCTTCTT 746
QY 242 TTACCTCAAGTGTGTAAA 261
Db 747 TTACCTCAAGTGTGTAAA 766

```

RESULT 11

```

US-10-238-443-13
; Sequence 13, Application US/10238443
; Publication No. US20030083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/198,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 13
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-238-443-13

```

```

Query Match 13.3%; Score 34.8; DB 14; Length 417;
Best Local Similarity 57.3%; Pred. No. 0.12;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 84 GAGGTGCAAAATGGACAGAGCCATCTCGTTATAGCGGCCGTGAAATATTTCCACGTTT 143
Db 220 GGGATGGGAGTGGATAAAGCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTTCCAGTCT 279
QY 144 TTTTCATGTTTCCGCAACAGGTCTCGCTGGTTGTGTCAGCGCATGGAGAGAC 193
Db 280 ATGGCTGGGTACTACCAAGGAGTCTGCGCGGGCTGCGGGATGGGAAGCC 329

```

```
RESULT 12
US-10-309-362-13
; Sequence 13, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 13
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: unknown
US-10-309-362-13

Query Match      13.3%; Score 34.8; DB 15; Length 417;
Best Local Similarity 57.3%; Pred. No. 0.12;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      84 GAGGTGCAATGGACAGACGCCATCTGCGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      220 GGGATGGGAGTGGATAAAGCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 279

Qy      144 TTTCATGGTTCCCAACAGGTGCTCGCTGTTGTGCGAGGATGGAGAGAC 193
Db      280 ATGGCTGGGTACTACCAAGAGTCTGCGCGGGCTGGCAGGGATGGGAAGCC 329

RESULT 13
US-10-238-443-11
; Sequence 11, Application US/10238443
; Publication No. US2003083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 11
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 330
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 360
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 394
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 440
; OTHER INFORMATION: unknown
```

```
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 465
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 478
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 508
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 530
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 538
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 557
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 580
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 595
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-10-238-443-11

Query Match      13.3%; Score 34.8; DB 14; Length 627;
Best Local Similarity 57.3%; Pred. No. 0.14;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      84 GAGGTGCAATGGACAGACGCCATCTGCGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      100 GGGATGGGAGTGGATAAAGCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 159

Qy      144 TTTCATGGTTCCCAACAGGTGCTCGCTGTTGTGCGAGGATGGAGAGAC 193
Db      160 ATGGCTGGGTACTACCAAGAGTCTGCGCGGGCTGGCAGGGATGGGAAGCC 209

RESULT 14
US-10-309-362-11
; Sequence 11, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 11
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 330
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 360
; OTHER INFORMATION: unknown
```

```
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 394
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 440
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 465
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 478
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 508
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 530
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 538
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 557
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 580
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 595
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-309-362-11
```

```
Query Match      13.3%; Score 34.8; DB 15; Length 627;
Best Local Similarity 57.3%; Pred. No. 0.14;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      84 GAGGTGCAATGGACAGAGCCATCTGCGTTATAGCGGCCGTGAAATATTTCCACGTTT 143
Db      100 GGGATGGGAGTGGATAAAGCCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 159

QY      144 TTTCATGGTTTCGCAACAGGTGTCGCGTGTGTCAGCGATGGAGAGAC 193
Db      160 ATGGCTGGGTACTACAGGAGTCTGCGCGGCTGGCAGGATGGGAAGCC 209
```

```
RESULT 15
US-10-238-443-10
; Sequence 10, Application US/10238443
; Publication No. US2003083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
```

```
; SEQ ID NO 10
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-238-443-10
```

```
Query Match      13.3%; Score 34.8; DB 14; Length 1710;
Best Local Similarity 57.3%; Pred. No. 0.21;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      84 GAGGTGCAATGGACAGAGCCATCTGCGTTATAGCGGCCGTGAAATATTTCCACGTTT 143
Db      1085 GGGATGGGAGTGGATAAAGCCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 1144

QY      144 TTTCATGGTTTCGCAACAGGTGTCGCGTGTGTCAGCGATGGAGAGAC 193
Db      1145 ATGGCTGGGTACTACAGGAGTCTGCGCGGCTGGCAGGATGGGAAGCC 1194
```

Search completed: August 27, 2005, 11:33:35
Job time : 479.968 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:00:48 ; Search time 311.984 Seconds
(without alignments)
4952.347 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 261
Sequence: 1 agccagcaagcgagcgagg.....tttacctcaagtggtgtaaa 261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.2	98.2	261	2 AAV15589	AAV15589 Human HPK
2	247.8	94.9	672	8 ACC51042	ACC51042 Human bla
3	247.8	94.9	672	8 ABX76400	ABX76400 Lung canc
4	247.8	94.9	672	11 ADN39021	ADN39021 Cancer/an
5	247.8	94.9	754	13 ADR26553	ADR26553 Breast ca
6	247.8	94.9	775	10 ADF60035	ADF60035 Human con
7	247.8	94.9	775	13 ADQ511654	ADQ511654 Human the
8	247.8	94.9	1026	2 AAV64572	AAV64572 Human Fan
9	247.8	94.9	1373	6 ABK92263	ABK92263 Prostate
10	247.8	94.9	1373	8 ABX76167	ABX76167 Lung canc
11	247.8	94.9	1373	11 ADN39435	ADN39435 Cancer/an
12	247.8	94.9	1705	13 ADQ87331	ADQ87331 Human tum
13	246.2	94.3	502	6 ABQ55843	ABQ55843 Human ova
14	233.6	89.5	1745	12 ADQ24412	ADQ24412 Human sof
15	175.8	67.4	748	13 ADS10353	ADS10353 Human the
16	137.8	52.8	516	10 ADF58395	ADF58395 Human pol
17	35.6	13.6	1065	4 AAS40959	AAS40959 cDNA enco
18	34.8	13.3	439	4 AAS41516	AAS41516 cDNA enco
19	34.8	13.3	1108	2 AA231913	AA231913 Human hel
20	34.8	13.3	1183	2 AA231920	AA231920 Human hel

21	34.8	13.3	1740	4 AAK94445	AAK94445 Human ful
22	34.8	13.3	1740	12 ADL31205	ADL31205 Full leng
23	34.8	13.3	1749	4 AAF87638	AAF87638 Human Rec
24	34.8	13.3	3159	13 ACN42473	ACN42473 Human dia
25	34.8	13.3	3703	4 AAF87636	AAF87636 Human Rec
26	34.8	13.3	3703	13 ADR83444	ADR83444 Human Rec
27	34.8	13.3	3707	2 AA231910	AA231910 Human hel
28	34.8	13.3	3715	4 AAF87637	AAF87637 Human Rec
29	34.8	13.3	3715	12 ADF83094	ADF83094 Human Rec
30	34.8	13.3	3879	13 ACN40275	ACN40275 Tumour-as
31	34.8	13.0	1260	12 ADH89535	ADH89535 Human Liv
32	33.8	13.0	1268	10 ACC72844	ACC72844 Human can
33	33.8	13.0	1268	13 ADS71346	ADS71346 Human liv
34	33.8	13.0	1322	10 ACC72843	ACC72843 Human can
35	33.8	13.0	1322	13 ADS71344	ADS71344 Human liv
36	33.8	13.0	1337	3 AAZ61210	AAZ61210 DNA enco
37	33.8	13.0	1363	3 AAA15007	AAA15007 cDNA enco
38	33.8	13.0	1376	4 AAF24856	AAF24856 Nucleotid
39	33.8	13.0	4810	12 ADH89542	ADH89542 Human Liv
40	33.6	12.9	2984	4 ABL25052	ABL25052 Drosophil
41	32	12.3	2000	8 ADA71938	ADA71938 Rice gene
42	31.8	12.2	2813	12 ADH10681	ADH10681 Mouse CX3
43	31.8	12.2	110000	12 ADN46845_05	Continuation (6 of
44	31.8	12.2	110000	12 ADN47591_15	Continuation (16 of
45	31.8	12.2	110000	12 ADN46123_05	Continuation (6 of

ALIGNMENTS

RESULT 1
AAV15589
ID AAV15589 standard; DNA; 261 BP.
XX
AC AAV15589;
XX
DT 02-JUL-1998 (first entry)
XX
DE Human HPK-1A C21.7 DNA.
XX
KW Cervical cancer; treatment; diagnosis; passage cell; lesion;
KW human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.
XX
OS Homo sapiens.
XX
PN DE19649207-C1.
XX
PD 26-FEB-1998.
XX
PF 27-NOV-1996; 96DE-01049207.
XX
PR 27-NOV-1996; 96DE-01049207.
XX
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Duerst M, Nees M;
XX
DR WPI; 1998-121623/12.
XX
PT Nucleic acid characteristic of late or early passage cells immortalised
PT by papilloma virus - and related polypeptide(s) and antibodies, used for
PT diagnosis and treatment of cervical cancer and assessing potential for
PT progression of cervical lesions.
XX
XX Claim 3; Fig 2; 8pp; German.
XX
PS This sequence, C21.7, is derived from a human papillomavirus (HPV)
XX immortalised human foreskin keratinocyte cell line HPK-1A and is
CC characteristic of late or early passage cells. This sequence is used in a
CC method for assessing the potential for progression of cervical lesions.
CC Antibodies generated against the encoded polypeptide are used for
CC diagnosis of cervical cancer and to assess potential for lesion
CC progression. Antibodies can also be used therapeutically by inhibiting

CC the polypeptide. Antisense molecules based on the nucleotide sequence are
CC used to inhibit expression of the protein. Detecting polypeptides, or
CC related RNA, characteristic of late passage cells (which are potentially
CC malignant) in cervical smears is a reliable way of assessing progression
CC potential

XX Sequence 261 BP; 69 A; 56 C; 77 G; 59 T; 0 U; 0 Other;

Query Match 98.2%; Score 256.2; DB 2; Length 261;
Best Local Similarity 98.9%; Pred. No. 8.6e-77;
Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCCAGCAACGACGAGGTCACAAATAGAGTGTGGTGCATGCTTGTGAGAGAAAC 60

Db 1 AGCCAGCAACGACGAGGTCACAAATAGAGTGTGGTGCATGCTTGTGAGAGAAAC 60

Qy 61 ACTTTCGAGTCCAGAACCCCAAGGAGGTGCAAAATGGACAGAGCCATCTGCGTTATAGCG 120

Db 61 ACTTTCGAGTCCAGAACCCCAAGGAGGTGCAAAATGGACAGAGCCATCTGCGTTATAGCG 120

Qy 121 GCCGTGAAATATTTCCACGTTTTTTCATGTTCCAAACAGGTGCTCCGCTGGTTGTGCA 180

Db 121 GCCGTGAAATATTTCCACGTTTTTTCATGTTCCAAACAGGTGCTCCGCTGGTTGTGCA 180

Qy 181 GCGATGGAGAGACCCCAAGCAGAGGAGGAGGTTTCTCTGGAGAGCCATGCCCTTC 240

Db 181 GCGATGGAGAGACCCCAAGCAGAGGAGGAGGTTTCTCTGGAGAGCCATGCCCTTC 240

Qy 241 TTTTACCTCAAGTGTGTAA 261

Db 241 TTTTACCTCAAGTGTGTAA 261

RESULT 2

ACC51042

ID ACC51042 standard; cDNA; 672 BP.

XX

AC ACC51042;

XX

DT 12-JUN-2003 (first entry)

XX

DE Human bladder cancer associated cDNA sequence SEQ ID NO:172.

XX

KW Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

XX

OS Homo sapiens;

XX

FN WO2003003906-A2.

XX

PD 16-JAN-2003.

XX

PF 03-JUL-2002; 2002WO-US021338.

XX

PR 03-JUL-2001; 2001US-0302814P.

XX

PR 03-AUG-2001; 2001US-0310099P.

XX

PR 08-NOV-2001; 2001US-0343705P.

XX

PR 13-NOV-2001; 2001US-0350666P.

XX

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Mack DH, Aziz N;

XX

XX WPI; 2003-201532/19.

DR

DR P-PSDB; ABR48226.

XX

XX Detecting a bladder cancer-associated transcript in a cell from a

PT patient, comprises contacting a biological sample from the patient with a

PT bladder cancer-associated polynucleotide or antibody.

XX

PS Claim 6; Page 289; 307pp; English.

XX

CC The present invention describes a method for detecting a bladder cancer-

CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications

XX Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;

Query Match 94.9%; Score 247.8; DB 8; Length 672;

Best Local Similarity 97.3%; Pred. No. 9.5e-74;

Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 CCAGCGAACCGACGAGGTCACAAATAGAGTGTGTGTCATGCTTGTGAGAGAAACAC 62

Db 267 CCAGCGAACCGACGAGGTCACAAATAGAGTGTGTGTCATGCTTGTGAGAGAAACAC 326

Qy 63 TTTTCGAGTCCAGAACCCCAAGGAGGTGCAAAATGGACAGAGCCATCTGCGTTATAGCGGC 122

Db 327 TTTTCGAGTCCAGAACCCCAAGGAGGTGCAAAATGGACAGAGCCATCTGCGTTATAGCGGC 386

Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGGTGCTCCGCTGGTTGTCAGC 182

Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGGTGCTCCGCTGGTTGTCAGC 446

Qy 183 GATGGAGAGACCCCAAGCAGAGGAGAACCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242

Db 447 GATGGAGAGACCCCAAGCAGAGGAGAACCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 506

RESULT 3

ABX76400

ID ABX76400 standard; DNA; 672 BP.

XX

AC ABX76400;

XX

DT 02-APR-2003 (first entry)

XX

DE Lung cancer-associated polynucleotide #264.

XX

KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX

OS Unidentified.

XX

PN WO200286443-A2.

XX

PD 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US012476.

XX

PR 18-APR-2001; 2001US-0284770P.

XX

PR 10-MAY-2001; 2001US-0290492P.

XX

PR 09-NOV-2001; 2001US-0339245P.

XX

PR 13-NOV-2001; 2001US-0350666P.

XX

PR 29-NOV-2001; 2001US-0334370P.

XX

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI: 2003-093161/08.
XX P-PSDB; ABUS6671.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
XX Claim 22; Page 392; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
XX invention
XX
XX Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;
SQ
Query Match 94.9%; Score 247.8; DB 8; Length 672;
Best Local Similarity 97.3%; Pred. No. 9.5e-74;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAAGCGGAGGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAACAC 62
DB 267 CCAGCGAAGCGGAGGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAACAC 326
QY 63 TTTTCGAGTCCAGAACCCCAAGGAGGTGCAATAGAGTGGTGTCTCATGCTGTGAGAGAG 122
DB 327 TTTTCGAGTCCAGAACCCCAAGGAGGTGCAATAGAGTGGTGTCTCATGCTGTGAGAGAG 386
QY 123 CGTGAATAATATTTCCACGTTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 182
DB 387 CGTGAATAATATTTCCACGTTTTTTTCATGTTTCGCAAGCAGTCTCGCTGGTTGTCAGC 446
QY 183 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 447 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 507 TTACCTCAAGTGTGTGAAA 525
RESULT 4
ADN39021
ID ADN39021 standard; cDNA; 672 BP.
XX
XX ADN39021;
XX
XX 17-JUN-2004 (first entry)
XX
XX Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:339.
XX
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-0355250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-0368809P.
XX 02-APR-2002; 2002US-0370110P.
XX 14-APR-2002; 2002US-0372246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397757P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX Mack DR, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI: 2003-468649/44.
XX P-PSDB; ADN39022.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 8; SEQ ID NO 339; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX antibodies and methods are useful for diagnosing, prognosing and treating
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX neovascularisation syndromes, scarring and uterine fibroids. They may
XX also be useful in wound healing and in contraception. The present
XX sequence represents a nucleic acid sequence of the invention.
XX
XX Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;
SQ
Query Match 94.9%; Score 247.8; DB 11; Length 672;
Best Local Similarity 97.3%; Pred. No. 9.5e-74;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAAGCGGAGGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAACAC 62
|||||
|||||

Db 267 CCAGCGAACGAGCGAGGTGACAAATAGAGTGTGGTGTTCATGTTTGTGAGAGAGAAACAC 326
QY 63 TTTCAGTGCAGAACCCAGAGGTGCAATAGGACAGACCATCTCGTTATAGCGGC 122
Db 327 TTTCAGTGCAGAACCCAGAGGTGCAATAGGACAGACCATCTCGTTATAGCGGC 386
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGTCAGC 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGTCAGC 446
QY 183 GATGAGAGACCCAGCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGAGAGACCCAGCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
QY 243 TTACTCTAAGTGTGTAA 261
Db 507 TTACTCTAAGTGTGTAA 525

RESULT 5
ADR26553/c
ID ADR26553 standard; DNA; 754 BP.
XX AC ADR26553;
XX DT 21-OCT-2004 (first entry)
XX DE Breast cancer prognosis marker #2414.
XX KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX OS Homo sapiens.
XX PN WO2004065545-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US001100.
XX PR 15-JAN-2003; 2003US-00342887.
XX PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX PA (NECA-) NETHERLANDS CANCER INST.
XX PI Van't Veer LJ, He Y;
XX DR WPI; 2004-593473/57.
XX CC Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX PS Disclosure; SEQ ID NO 2414; 226pp; English.
XX CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
SQ Sequence 754 BP; 150 A; 245 C; 206 G; 153 T; 0 U; 0 Other;
Query Match 94.9%; Score 247.8; DB 13; Length 754;
Best Local Similarity 97.3%; Pred No. 1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGAGCGGTGACAAATAGAGTGTGGTGTTCATGTTTGTGAGAGAGAAACAC 62
|||||

Db 498 CCAGCGAACGAGCGGTGACAAATAGAGTGTGGTGTTCATGTTTGTGAGAGAGAAACAC 439
QY 63 TTTCAGTGCAGAACCCAGAGGTGCAATAGGACAGACCATCTCGTTATAGCGGC 122
Db 438 TTTCAGTGCAGAACCCAGAGGTGCAATAGGACAGACCATCTCGTTATAGCGGC 379
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGTCAGC 182
Db 378 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTGTGTCAGC 319
QY 183 GATGAGAGACCCAGCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 318 GATGAGAGACCCAGCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 259
QY 243 TTACTCTAAGTGTGTAA 261
Db 258 TTACTCTAAGTGTGTAA 240
RESULT 6
ADF60035
ID ADF60035 standard; cDNA; 775 BP.
XX AC ADF60035;
XX DT 12-PEB-2004 (first entry)
XX DE Human contig polynucleotide sequence SEQ ID NO:2402.
XX KW biological activity; genetic engineering; hybridisation probe; oligomer;
KW primer; chromosome mapping; gene mapping; recombinant protein production;
KW human; gene; ss.
XX OS Homo sapiens.
XX PN WO2003080795-A2.
XX PD 02-OCT-2003.
XX PF 09-AUG-2002; 2002WO-US025485.
XX PR 09-AUG-2001; 2001US-0311261P.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
XX DR WPI; 2003-876918/81.
XX DR P-PSDB; ADF60487.
XX PT New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.
XX PS Example 2; SEQ ID NO 2402; 571pp; English.
XX CC The present invention describes isolated polynucleotide sequences (I),
CC which encode polypeptides (II) with biological activity. Also described:
CC (1) a vector comprising (I); (2) an expression vector comprising (I); (3)
CC a host cell genetically engineered to comprise (I) which is operatively
CC associated with a regulatory sequence that modulates expression of (I) in
CC the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition
CC comprising the polypeptide of (4) and a carrier; (6) an antibody directed
CC against the polypeptide of (4); (7) detecting (I) or the polypeptide of
CC (4) in a sample; (8) identifying a compound that binds to the polypeptide
CC of (4); (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA. The
CC present sequence represents a human contig polynucleotide sequence, which
CC is used in an example from the present invention.
XX

```
SQ Sequence 775 BP; 164 A; 209 C; 250 G; 152 T; 0 U; 0 Other;
Query Match          94.9%; Score 247.8; DB 10; Length 775;
Best Local Similarity 97.3%; Pred. No. 1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAACAC 62
DB 267 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAACAC 326
QY 63 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCATCTCGGTTATAGCGGC 122
DB 327 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCATCTCGGTTATAGCGGC 386
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTGTCTCGGTTATAGCGGC 182
DB 387 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTGTCTCGGTTATAGCGGC 446
QY 183 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242
DB 447 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 506
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 507 TTACCTCAAGTGTGTGAAA 525

RESULT 7
ADSI1654
ID ADSI1654 standard; DNA; 775 BP.
AC ADSI1654;
DT 16-DEC-2004 (first entry)
DE Human therapeutic contig DNA - SEQ ID 1891.
DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
KW inflammatory; haematopoesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
OS Homo sapiens.
PN WO2004080148-A2.
XX 23-SEP-2004.
XX 30-SEP-2003; 2003WO-US030720.
XX 02-OCT-2002; 2002US-0416186P.
XX (NUVE-) NUVELO INC.
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
DR WPI; 2004-668857/65.
DR P-PSDB; ADSI2252.
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX Example 2; SEQ ID NO 1891; 718pp; English.
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnery activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
```

```
CC DNA of the invention. The current sequence is not shown explicitly within
CC the specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 775 BP; 164 A; 209 C; 250 G; 152 T; 0 U; 0 Other;
Query Match          94.9%; Score 247.8; DB 13; Length 775;
Best Local Similarity 97.3%; Pred. No. 1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAACAC 62
DB 267 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGCTTGTGAGAGAGAAACAC 326
QY 63 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCATCTCGGTTATAGCGGC 122
DB 327 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCATCTCGGTTATAGCGGC 386
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTGTCTCGGTTATAGCGGC 182
DB 387 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTGTCTCGGTTATAGCGGC 446
QY 183 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242
DB 447 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 506
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 507 TTACCTCAAGTGTGTGAAA 525

RESULT 8
AAV64572
ID AAV64572 standard; DNA; 1026 BP.
AC AAV64572;
DT 27-JAN-1999 (first entry)
DE Human Fanconi anaemia-associated gene II DNA.
DE Fanconi anaemia gene II; immunogen; diagnosis; detection; disease;
KW cell cycle; disorder; cell activation; DNA repair; cytopaenia;
KW gene therapy; tumorigenesis; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 256..927
XX FT /*tag= a
XX FT /product= "Fanconi anaemia gene II"
XX FT /note= "long reading frame"
XX CDS 430..927
XX FT /*tag= b
XX FT /product= "Fanconi anaemia gene II"
XX FT /note= "short reading frame"
XX
XX WO9845428-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98WO-EP001994.
XX
XX 07-APR-1997; 97EP-00105688.
XX
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX Kubbies M, Machl A, Planitzer S;
XX WPI; 1998-568348/48.
XX P-PSDB; AAW81754.
XX New human Fanconi anaemia associated gene-II - useful for diagnosis,
XX treatment and prevention of diseases associated with abnormal cell
```

PT cycling or activation, DNA repair, cytopaenia, tumorigenesis etc.
PS Claim 1; Page 18-19; 35pp; German.
XX
CC This sequence encodes a protein which is associated with Fanconi anaemia.
CC This protein can be used as an immunogen for preparation of antibodies.
CC This sequence can be used for diagnosis of, or detecting predisposition
CC to diseases that involve disorders of the cell cycle, cell activation,
CC cell cycle progression, DNA repair, cytopaenia, tumorigenesis and/or
CC tumour progression, also for treatment and prevention of these diseases,
CC particularly by gene therapy
XX
SQ Sequence 1026 BP; 201 A; 301 C; 331 G; 191 T; 0 U; 2 Other;
Query Match 94.9%; Score 247.8; DB 2; Length 1026;
Best Local Similarity 97.3%; Pred. No. 1.1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62
Db 522 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 581
QY 63 TTTCGAGTGCCAGAACCCAGGAGGTGCAATGAGAGCCATACCTGCTTATAGCGGC 122
Db 582 TTTCGAGTGCCAGAACCCAGGAGGTGCAATGAGAGCCATACCTGCTTATAGCGGC 641
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 182
Db 642 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 701
QY 183 GATGAGAGACCCAGCGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 702 GATGAGAGACCCAGCGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 761
QY 243 TTACTCTCAAGTGTGTGAAA 261
Db 762 TTACTCTCAAGTGTGTGAAA 780
RESULT 9
ABK92263
ID ABK92263 standard; DNA; 1373 BP.
XX
AC ABK92263;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #149.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 06-APR-2001; 2001US-0276888P.
PR 24-APR-2001; 2001US-0281922P.
PR 30-APR-2001; 2001US-0286214P.
PR 04-MAY-2001; 2001US-00847046.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX

PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61944.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 426; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1373 BP; 346 A; 324 C; 376 G; 327 T; 0 U; 0 Other;
Query Match 94.9%; Score 247.8; DB 6; Length 1373;
Best Local Similarity 97.3%; Pred. No. 1.3e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62
Db 136 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 195
QY 63 TTTCGAGTGCCAGAACCCAGGAGGTGCAATGAGAGCCATACCTGCTTATAGCGGC 122
Db 196 TTTCGAGTGCCAGAACCCAGGAGGTGCAATGAGAGCCATACCTGCTTATAGCGGC 255
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 182
Db 256 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 315
QY 183 GATGAGAGACCCAGCGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 316 GATGAGAGACCCAGCGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 375
QY 243 TTACTCTCAAGTGTGTGAAA 261
Db 376 TTACTCTCAAGTGTGTGAAA 394
RESULT 10
ABX76167
ID ABX76167 standard; DNA; 1373 BP.
XX
AC ABX76167;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #39.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.

XX WO200286443-A2.
XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US012476.
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX P-PSDB; ABUS6446.
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX Claim 22; Page 219-220; 453pp; English.
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
XX invention
XX SQ Sequence 1373 BP; 346 A; 324 C; 376 G; 327 T; 0 U; 0 Other;
Query Match 94.9%; Score 247.8; DB 8; Length 1373;
Best Local Similarity 97.3%; Pred. No. 1.3e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACCGGACGAGGGTGACAAATAGAGTGTGTGTCTCATGTGTGTGAGAGAGAAACAC 62
Db 136 CCAGCGAACCGGACGAGGGTGACAAATAGAGTGTGTGTCTCATGTGTGTGAGAGAGAAACAC 195
QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGAGCAGAGCCATACCTGGTTATAGCGGC 122
Db 196 TTTCGAGTGCAGAACCCAGGAGGTGCAATGAGCAGAGCCATACCTGGTTATAGCGGC 255
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGACAGGTGCTCGCTGTTGTCGACG 182
Db 256 CGTGAATAATTTCCACGTTTTTTCATGTTTCGAAAGCAGTGTCCGCTGGTTGTCGACG 315
QY 183 GATGGAGAGACCCAGCCAGAGGAGGCGTTTCTTCGGAAGAGCCCATGCCCTTCTT 242
Db 316 GATGGAGAGACCCAGCCAGAGGAGGCGTTTCTTCGGAAGAGCCCATGCCCTTCTT 375
QY 243 TTACTTCAAGTGTGTGAAA 261
Db 376 TTACTTCAAGTGTGTGAAA 394

RESULT 11

ADN39435
ID ADN39435 standard; cDNA; 1373 BP.
XX
AC ADN39435;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A35.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW inflammatory disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 18-FEB-2002; 2002US-0355250P.
XX 03-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-036809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-0372246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
XX P-PSDB; ADN39436.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 8; SEQ ID NO A35; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX antibodies and methods are useful for diagnosing, prognosing and treating

ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antineoplastic; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19.

P-PSDB; ABP42766.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 1; SEQ ID NO 1723; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a cDNA encoding a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 502 BP; 112 A; 125 C; 152 G; 113 T; 0 U; 0 Other;

Query Match 94.3%; Score 246.2; DB 6; Length 502;

Best Local Similarity 96.9%; Pred. No. 2.9e-73;

Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

3 CCAGCGAAGCGAGGGTGCAATAGAGTGGTGTCTGCTGTGTGAGAGAGAAACAC 62

85 CCAGCGAAGCGAGGGTGCAATAGAGTGGTGTCTGCTGTGTGAGAGAGAAACAC 144

63 TTTCGAGTCCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 122

145 TTTCGAGTCCAGAACCCAGGAGGTGCAATGGACAGAGCCGTTACTGCTTATAGCGGC 204

123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGGTGGTGTGACAGC 182

205 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGGTGGTGTGACAGC 264

183 GATGGAGAGACCCAGGAGGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242

265 GATGGAGAGACCCAGGAGGAGAGCGGTTTCTCTGGAAGAGCCATGCCCTTCTT 324

243 TTACCTCAAGTGTGTAATA 261

325 TTACCTCAAGTGTGTAATA 343

RESULT 14

ADQ24412

ID ADQ24412 standard; DNA; 1745 BP.

XX AC ADQ24412;

XX DT 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7232.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; ds.

KW Homo sapiens.

OS WO2004048938-A2.

PN 10-JUN-2004.

PD 26-NOV-2003; 2003WO-US038193.

PF 26-NOV-2002; 2002US-0429739P.

PR (PROT-) PROTEIN DESIGN LABS INC.

PA Aziz N, Ginsburg WM, Zlotnik A;

PI WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 7232; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the CC specification per se but was submitted in CD format by the inventor.

XX Sequence 1745 BP; 402 A; 455 C; 511 G; 377 T; 0 U; 0 Other;

Query Match 89.5%; Score 233.6; DB 12; Length 1745;

Best Local Similarity 96.2%; Pred. No. 9.9e-69;

Matches 250; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 3 CCAGCGAACGCGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 62
Db 507 CCAGCGAACGCGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 566
Qy 63 -TTTCGAGTGCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTGCGTTATAGCGG 121
Db 567 TTTCGAATGCGAGAACCCAGGAGGTGCAATATGACAGAGCCATCTGCGTTATAGCGG 626
Qy 122 CCGTGAAATATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAG 181
Db 627 CCGTGAAATATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAG 686
Qy 182 CGATGGAGAGCCCAAGCCAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCT 241
Db 687 CGATGGAGAGCCCAAGCCAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCT 746
Qy 242 TTACCTCAAGTGTGTGTA 261
Db 747 TTACCTCAAGTGTGTGTA 766

RESULT 15
ADS10353
ID ADS10353 standard; DNA; 748 BP.
XX ADS10353;
AC ADS10353;
DT 16-DEC-2004 (first entry)
DE Human therapeutic DNA - SEQ ID 590.
XX
XX antinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI; 2004-668857/65.
DR P-PSDB; ADS11037.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX
XX Claim 1; SEQ ID NO 590; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
XX Sequence 748 BP; 157 A; 207 C; 246 G; 138 T; 0 U; 0 Other;

Query Match 67.4%; Score 175.8; DB 13; Length 748;
Best Local Similarity 85.7%; Pred. No. 3.5e-49;
Matches 222; Conservative 0; Mismatches 2; Indels 35; Gaps 1;
Qy 3 CCAGCGAACGCGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 62
Db 278 CCAGCGAGCGAGCGAGGTTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 337
Qy 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTGCGTTATAGCGG 122
Db 338 TTTCGAGTGCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTGCGTTATAGCGG 397
Qy 123 CGTGAAATATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAGC 182
Db 398 CGTGA-----TGCTCCGCTGTTGCGAGC 422
Qy 183 GATGGAGAGACCCCAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 423 GATGGAGAGACCCCAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 482
Qy 243 TTACCTCAAGTGTGTGTA 261
Db 483 TTACCTCAAGTGTGTGTA 501

Search completed: August 27, 2005, 08:59:49
Job time : 313.984 secs

GenCore version 5.1.6
; Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:48:34 ; Search time 93.5484 Seconds
(without alignments)
4565.212 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 261

Sequence: 1 agccagcgaacgagcagg.....tttactctcaagtgtgtataa 261

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2.6/prodata/1/ina/5A COMB.seq:*
- 2: /cgn2.6/prodata/1/ina/5B COMB.seq:*
- 3: /cgn2.6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2.6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2.6/prodata/1/ina/PCUS COMB.seq:*
- 6: /cgn2.6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	100.0	261	3	US-09-308-984-2
2	35.6	13.6	399	4	US-09-621-976-8976
3	34.8	13.3	1233	4	US-09-949-016-13456
4	33.8	13.0	1260	4	US-09-949-016-1949
5	33.8	13.0	1337	4	US-09-127-928-1
6	33.8	13.0	8572	4	US-09-949-016-13691
7	31.2	12.0	114793	4	US-10-148-806-3
8	30.6	11.7	251769	4	US-09-949-016-13185
9	30.6	11.7	251769	4	US-09-949-016-13186
10	30.6	11.7	266748	4	US-09-949-016-13187
11	30.6	11.7	266748	4	US-09-949-016-13188
12	30.4	11.6	5157	2	US-08-474-169-7
13	30.4	11.6	87470	4	US-09-949-016-15881
14	30.2	11.6	144362	4	US-09-949-016-16066
15	30.2	11.6	784019	4	US-09-949-016-14033
16	30.2	11.6	828152	4	US-09-949-016-12777
17	30	11.5	601	4	US-09-949-016-14114
18	30	11.5	1541	4	US-09-270-767-11220
19	30	11.5	9386	4	US-09-949-016-15739
20	29.8	11.4	632	1	US-08-580-038-65
21	29.6	11.3	735	4	US-09-328-352-1496
22	29.6	11.3	1550	4	US-09-976-594-766
23	29.4	11.3	1512	4	US-09-107-532A-54
24	29.4	11.3	49225	4	US-09-902-540-1269
25	29	11.1	289	3	US-09-5007-005-17
26	29	11.1	289	3	US-09-244-796-17
27	29	11.1	1313	4	US-09-023-655-59

C	28	29	11.1	5860	3	US-09-221-017B-820	Sequence 820, Appl
C	29	28.8	11.0	480	4	US-09-621-976-10615	Sequence 10615, A
C	30	28.8	11.0	6337	4	US-09-620-312D-1063	Sequence 1063, Ap
C	31	28.6	11.0	3001	4	US-09-539-333D-221	Sequence 221, Appl
C	32	28.4	10.9	1116	4	US-10-265-012-13	Sequence 13, Appl
C	33	28.4	10.9	1302	4	US-10-265-012-9	Sequence 9, Appl
C	34	28.4	10.9	1521	4	US-10-265-012-11	Sequence 11, Appl
C	35	28.4	10.9	1707	4	US-10-265-012-7	Sequence 7, Appl
C	36	28.4	10.9	1824	4	US-10-265-012-1	Sequence 1, Appl
C	37	28.4	10.9	30337	4	US-09-949-016-13053	Sequence 13053, A
C	38	28.4	10.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C	39	28.2	10.8	601	4	US-09-949-016-203508	Sequence 203508,
C	40	28.2	10.8	4584	2	US-08-901-200A-15	Sequence 15, Appl
C	41	28.2	10.8	4584	3	US-09-219-391-15	Sequence 15, Appl
C	42	28.2	10.8	6418	1	US-08-480-528A-11	Sequence 11, Appl
C	43	28.2	10.8	6418	1	US-08-479-666-11	Sequence 11, Appl
C	44	28.2	10.8	6418	5	PCT-US93-10520-11	Sequence 11, Appl
C	45	28.2	10.8	56976	4	US-09-949-016-17486	Sequence 17486, A

ALIGNMENTS

RESULT 1

US-09-308-984-2

; Sequence 2, Application US/09308984

; Patent No. 6388055

; GENERAL INFORMATION:

; APPLICANT: Durest, Matthias

; APPLICANT: Nees, Matthias

; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS

; FILE REFERENCE: SCHU 204 (09902857)

; CURRENT APPLICATION NUMBER: US/09/308,984

; CURRENT FILING DATE: 1999-09-03

; PRIOR APPLICATION NUMBER: PCT/DE97/02660

; PRIOR FILING DATE: 1996-11-12

; PRIOR APPLICATION NUMBER: DE 196 49207

; PRIOR FILING DATE: 1997-11-27

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 2

; LENGTH: 261

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-308-984-2

Query Match 100.0%; Score 261; DB 3; Length 261;

Best Local Similarity 100.0%; Pred. No. 3.5e-82;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCAGCGAAGCGAGGGTGCAATAGAGTGTGTCTCATGCTGTGAGAGAGAAAC 60

DB 1 AGCCAGCGAAGCGAGGGTGCAATAGAGTGTGTCTCATGCTGTGAGAGAGAAAC 60

QY 61 ACTTTCGAGTCCCAAGACCCCAAGAGGTCGCAATGGACAGAGCCATCTCGGTTATAGCG 120

DB 61 ACTTTCGAGTCCCAAGACCCCAAGAGGTCGCAATGGACAGAGCCATCTCGGTTATAGCG 120

QY 121 GCCGTGAAATATTTCCACGTTTTTCATGTTGCAACAGTGTCTCGCTGTTGTGCA 180

DB 121 GCCGTGAAATATTTCCACGTTTTTCATGTTGCAACAGTGTCTCGCTGTTGTGCA 180

QY 181 CGCATGGAGAGACCCCAAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTC 240

DB 181 CGCATGGAGAGACCCCAAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTC 240

QY 241 TTTTACCTCAAGTGTGTGAAA 261

DB 241 TTTTACCTCAAGTGTGTGAAA 261

RESULT 2

US-09-621-976-8976

; Sequence 8976, Application US/09621976

```
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054P2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match
Best Local Similarity 13.6%; Score 35.6; DB 4; Length 399;
Matches 29; Conservative 108; Mismatches 97; Indels 0; Gaps 0;

QY 10 ACGACGAGGTGCAATAGATGGTGTCTATGCTGTGAGAGAGAAACACTTTCGAG 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 WKKRRRRRRWWWWKSMCMWKKSKSWRSWGMTRKMKGRGAASWAGYMSMTYMTTRW 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 TCCGAAACCCAGGAGGTGCAATGCGACAGAGCCACTACTGCTTATAGCGCCGTGAA 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 RYRYRKAKTWRAGAGMGMKAGNAMAAYAKWYMAWRRTAMKYWMMKSKSKSMRRRAW 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ATATTCCACGTTTTTTTCATGGTGTGCCAACAGGTGCTCGCTGGTGTGCGACGATGGAG 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 YAWMYMMARRTWGMRASCYRGAYWASAGMYMMYMMYMMRKKWYSAGWSNWKWTRRC 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 AGACCAACCCAGAGAGAGAGCGGTTCCTCTCGAAGAGCCCATGCCCTTCTTT 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 ASYSCSSSYCMWAKMMYWKTSRWSYYSYRCTKYRRSCCWSMVCWKTY 273

RESULT 3
US-09-949-016-3456
; Sequence 3456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3456
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3456

Query Match
Best Local Similarity 57.3%; Score 34.8; DB 4; Length 1233;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 84 GAGGTCCAAATGACAGAGCCACTACTGCGTGTATAGCGCGCGTGAATAATTTCCAGTTT 143
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 958 GGGATGGGAGTGGATTAAGCCATGTCAGGTGTGTCGCCCATGGATATTCGCAAGTCT 1017
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 TTTCATGGTTGCAACAGGTGCTCCGCTGTGTGCGAGCGATGGAGAGAC 193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054P2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match
Best Local Similarity 12.4%; Score 35.6; DB 4; Length 399;
Matches 29; Conservative 108; Mismatches 97; Indels 0; Gaps 0;

QY 10 ACGACGAGGTGCAATAGATGGTGTCTATGCTGTGAGAGAGAAACACTTTCGAG 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 WKKRRRRRRWWWWKSMCMWKKSKSWRSWGMTRKMKGRGAASWAGYMSMTYMTTRW 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 TCCGAAACCCAGGAGGTGCAATGCGACAGAGCCACTACTGCTTATAGCGCCGTGAA 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 RYRYRKAKTWRAGAGMGMKAGNAMAAYAKWYMAWRRTAMKYWMMKSKSKSMRRRAW 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ATATTCCACGTTTTTTTCATGGTGTGCCAACAGGTGCTCGCTGGTGTGCGACGATGGAG 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 YAWMYMMARRTWGMRASCYRGAYWASAGMYMMYMMYMMRKKWYSAGWSNWKWTRRC 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 AGACCAACCCAGAGAGAGCGGTTCCTCTCGAAGAGCCCATGCCCTTCTTT 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 ASYSCSSSYCMWAKMMYWKTSRWSYYSYRCTKYRRSCCWSMVCWKTY 273

RESULT 3
US-09-949-016-3456
; Sequence 3456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3456
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3456

Query Match
Best Local Similarity 57.3%; Score 34.8; DB 4; Length 1233;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 84 GAGGTCCAAATGACAGAGCCACTACTGCGTGTATAGCGCGCGTGAATAATTTCCAGTTT 143
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 958 GGGATGGGAGTGGATTAAGCCATGTCAGGTGTGTCGCCCATGGATATTCGCAAGTCT 1017
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 TTTCATGGTTGCAACAGGTGCTCCGCTGTGTGCGAGCGATGGAGAGAC 193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054P2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match
Best Local Similarity 13.0%; Score 33.8; DB 4; Length 1260;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 94 TGGACAGAGCCACTACTGCTGTATAGCGCGCGTGAATAATTTCCACGTTTTTTCATGTT 153
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 151 TGGTCAGAGCCAGTGTTCCTCCATGGGACCTAAAGACAGTGCCCAAGTGCCTGCACCGTG 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 154 CGCAACAGGTCTCGCTGGTGTGTCAGCGATGGAGAGACCCCAAGCCAGAGGAGAGCGG 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 211 GACCACAGCGAGCCACTGGCGCGGTGATGTCCACGAGGCGCTGTGACCCC 270
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 TTTCTCTGGAAG 226
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 271 GCTCTCTGGCAG 283
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-127-928-1
; Sequence 1, Application US/09127928
; Patent No. 6472172
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
; FILE REFERENCE: Protein
; FILE REFERENCE: DNA Encoding HIAP3
; CURRENT APPLICATION NUMBER: US/09/127,928
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1066)
US-09-127-928-1

Query Match
Best Local Similarity 53.4%; Score 33.8; DB 4; Length 1337;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054P2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match
Best Local Similarity 12.4%; Score 35.6; DB 4; Length 399;
Matches 29; Conservative 108; Mismatches 97; Indels 0; Gaps 0;

QY 10 ACGACGAGGTGCAATAGATGGTGTCTATGCTGTGAGAGAGAAACACTTTCGAG 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 WKKRRRRRRWWWWKSMCMWKKSKSWRSWGMTRKMKGRGAASWAGYMSMTYMTTRW 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 TCCGAAACCCAGGAGGTGCAATGCGACAGAGCCACTACTGCTTATAGCGCCGTGAA 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 RYRYRKAKTWRAGAGMGMKAGNAMAAYAKWYMAWRRTAMKYWMMKSKSKSMRRRAW 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ATATTCCACGTTTTTTTCATGGTGTGCCAACAGGTGCTCGCTGGTGTGCGACGATGGAG 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 YAWMYMMARRTWGMRASCYRGAYWASAGMYMMYMMYMMRKKWYSAGWSNWKWTRRC 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 AGACCAACCCAGAGAGAGCGGTTCCTCTCGAAGAGCCCATGCCCTTCTTT 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 ASYSCSSSYCMWAKMMYWKTSRWSYYSYRCTKYRRSCCWSMVCWKTY 273
```

[illegible]

```

RESULT 6
US-09-949-016-13691
; Sequence 13691, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13691
; LENGTH: 8572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13691

```

Query Match	13.0%	Score 33.8;	DB 4;	Length 8572;
Best Local Similarity	53.4%;	Pred. No. 0.46;		
Matches	71;	Conservative 0;	Mismatches 62;	Indels 0; Gaps 0;
Qy	94	TGGACAGAGCCATACTCGGTTATAGCGCGCGTGAARATATTTCCACGTTTTTTCATGGTT	153	
Db	2151	TGGTCAGAGCGAGTGTTCCTCCATGGAGCCTAAAGACAGTGCACAGTGCTGCACCGTG	2210	
Qy	154	CGCAACAGGTGCTCCGCTGGTGTGTGCAGCGATGGAGAGACCCAGCCAGGAGGAAGCGG	213	
Db	2211	GACCACAGCCGACCATGGCGACCGGTGATGTGTCCACGCAGGAGCGTGTGGACCCC	2270	
Qy	214	TTTCTCTCTGGAAG	226	
Db	2271	GCTCTCTGGGCAG	2283	

```

RESULT 7
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

```

	Query Match	12.0%;	Score 31.2;	DB 4;	Length 114793;
	Best Local Similarity	58.7%;	Pred. No. 14;	Mismatches 0;	Gaps 0;
	Matches 54;	Conservative		Indels 38;	
Qy	147	CATGGTTCCGACAGGTGCTCCGCTGGTTGTGTCACGGATGAGAGACCCACAGCCACGAGA	206		
Db	43606	CCTGGTAGGCAACGGAGCGCTCTTTGCCATTGCAGGGATGAAGCCACCGAGCGAGGGAGA	43665		
Qy	207	GAAGCGGTTTCTCTCGAAGAGCCCATGCCCCT	238		
Db	43666	AAAGTGTCTTTGCCCTACAAGCAACTAAGTCAT	43697		

RESULT 8
US-09-949-016-13185/c
; Sequence 13185, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13185
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13185

	Query Match	11.7%	Score 30.6;	DB 4;	Length 251769;
	Best Local Similarity	52.8%;	Pred. No. 34;		
	Matches	66;	Conservative 0;	Mismatches 59;	Indels 0; Gaps 0;
Qy	36	GTGTCATGCTTGTGAGAGAGNAAACACTTTCGAGTGCAGAACCCAGAGGTGCAAAATG	95		
Db	218276	GTATCTTGAATTACACAGATATACTATTTTCAGAGCAGAAGAAAGAGAGGGGACAATAAA	218217		
Qy	96	GACAGGCCCATCTACGCGTTATAGCGGCGTGAATAATTTCCACGTTTTTTTCATCGTTTCG	155		
Db	218216	CAAGAGTAGTCTGTCATAAATGAGCAATACTAGTTCTCTTTTGGCATCAGAGAAG	218157		
Qy	156	CAACA 160			
Db	218156	AAACA 218152			

RESULT 9
US-09-949-016-13186/c
? Sequence 13186, Application US/09949016
? Patent No. 6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001307
? CURRENT APPLICATION NUMBER: US/09/949.016
? CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13186
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13186

Query Match 11.7%; Score 30.6; DB 4; Length 251769;
Best Local Similarity 52.8%; Pred. No. 34;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACCTTTCGAGTGCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218276 GTATCTTGATTCATACAGATATACTATTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218217

QY 96 GACAGAGCCATCTCGGTTATAGCGCGGTGAAAATATTTCCACGTTTTTTCATGGTTTCG 155
DB 218216 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218157

QY 156 CAACA 160
DB 218156 AAACA 218152

RESULT 10
US-09-949-016-13187/c
; Sequence 13187, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13187
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13187

Query Match 11.7%; Score 30.6; DB 4; Length 266748;
Best Local Similarity 52.8%; Pred. No. 35;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACCTTTCGAGTGCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218241 GTATCTTGATTCATACAGATATACTATTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218182

QY 96 GACAGAGCCATCTCGGTTATAGCGCGGTGAAAATATTTCCACGTTTTTTCATGGTTTCG 155
DB 218181 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218122

QY 156 CAACA 160
DB 218121 AAACA 218117

RESULT 11
US-09-949-016-13188/c
; Sequence 13188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13188
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13188

Query Match 11.7%; Score 30.6; DB 4; Length 266748;
Best Local Similarity 52.8%; Pred. No. 35;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACCTTTCGAGTGCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218241 GTATCTTGATTCATACAGATATACTATTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218182

QY 96 GACAGAGCCATCTCGGTTATAGCGCGGTGAAAATATTTCCACGTTTTTTCATGGTTTCG 155
DB 218181 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218122

QY 156 CAACA 160
DB 218121 AAACA 218117

RESULT 12
US-08-474-169-7
; Sequence 7, Application US/08474169
; Patent No. 5851796
; GENERAL INFORMATION:
; APPLICANT: Schatz, David G.
; TITLE OF INVENTION: An Autoregulatory Tetracycline-Regulated
; FILE OF INVENTION: System for Inducible Gene Expression in Eucaryotes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,169
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5157 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 502..2184
; US-08-474-169-7

```

```

Query Match      11.6%; Score 30.4; DB 2; Length 5157;
Best Local Similarity 54.5%; Pred. No. 5.7; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 51;

QY 131 TATTTCCAGCTTTTTCATGTTTGGCAACAGGTGCTCCGCTGTTGTGCGAGCGATGGAGA 190
Db 3047 TTGTGCCAACTCATCAATGATATCATGTCGCTCTAGAGCTGCATTAAATGATC 3106

QY 191 GACCCAGCCAGAGGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 3107 GGCACACGCGGGGAGAGCGGTTTTCGTATTGGCGCTCTTCGCTTCT 3158

```

```

RESULT 13
US-09-949-016-15881
; Sequence 15881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15881
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(87470)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15881

```

```

Query Match      11.6%; Score 30.4; DB 4; Length 87470;
Best Local Similarity 49.4%; Pred. No. 24; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 81;

QY 91 AAATGACAGAGCCATACCTGCTGTTAGCGGCGGTGAAATATTTCCAGTTTTCATG 150
Db 17392 AAATGTTCAAGTGATACCTAGTTTAACTGCTTGCATGCTCTTTTGTGTTTTT 17451

QY 151 GTTCGCAACAGGTGCTCCGCTGTTGTGCGAGCGATGGAGAGCCCAAGCCAGGAGAAG 210
Db 17452 GACACAGGCTCTGCTGCTGTTGCCAGGCTGGAGTGCAGTGGCACAATCTCAGCTTACTG 17511

QY 211 CGGTTTCTCTGGAAGAGCCCATGCCCTCTTTTACCTCA 250
Db 17512 CAGCCTCTGCTCCAGGTTTCAAGCAATTTCTCCACCTCA 17551

```

```

RESULT 14
US-09-949-016-16066
; Sequence 16066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16066
; LENGTH: 144362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(144362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16066

```

```

Query Match      11.6%; Score 30.2; DB 4; Length 144362;
Best Local Similarity 58.2%; Pred. No. 36; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 38;

QY 27 TAGAGTGTGGTTCATGTTGTGAGAGAGAAACAACCTTCGAGTCCCAAGGAG 86
Db 27633 TTGAATTTGGTGTATGTTTCATGTTAGAGCCCAACAGGATTTACTGTTAGATAGGTAAGG 27692

QY 87 GTGCAATGGACAGAGCCATCTCGTTTATA 117
Db 27693 GTGTAAGAGGAGTCAAGCATATCTGTGTAAGA 27723

```

```

RESULT 15
US-09-949-016-14033/c
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

```

```

Query Match      11.6%; Score 30.2; DB 4; Length 784019;
Best Local Similarity 51.1%; Pred. No. 82; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 68;

QY 17 AGGTTGACAATAGAGTGTGTTGTCATGCTTGTGAGAGAGAAACAACCTTCGAGTCCCAAG 76
Db 326015 AGGTTGAAACAAGAGGAGTGTAAATGCTAGAAATTTACCAATCAGTACACAGGCTCAGT 325956

```

Qy 77 ACCCAAGGAGTGC AANTGCACAGAGCCATACTGCGTTATAGCGGCCCGTGAATAATTTTC 136
Db 325955 AACCAATGAACTCTCATAGGAATATCAATAAAGCATTTCAGAAACACTAAAAATAATTTC 325896
Qy 137 CACGTTTTTTCATGGTTTCG 155
Db 325895 CTTCTCCAACTTTTCTCG 325877

Search completed: August 27, 2005, 11:37:10
Job time : 98.5484 secs

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)